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From: Whiteman, Brian  
Sent: Wednesday, January 11, 2006 6:27 PM  
To: STIC-Biotech/ChemLib  
Subject: seq search

10/822873

SEQ ID NO: 10 and 11

- 1) us patents and published us patent applications
- 2) commercial databases

Thanks

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Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

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Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: 1/23  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 19:44:52 ; Search time 23 Seconds  
(without alignments)  
363.054 Million cell updates/sec

Title: US-10-822-873-11  
Perfect score: 551  
Sequence: 1 WTGSTIAPTDTYNTATG.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5\_COMB.pep.\*  
2: /cgn2\_6/prodata/1/iaa/6\_COMB.pep.\*  
3: /cgn2\_6/prodata/1/iaa/H\_COMB.pep.\*  
4: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep.\*  
5: /cgn2\_6/prodata/1/iaa/RE\_COMB.pep.\*  
6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

				SUMMARIES	
Result No.	Score	Query Match	Length DB ID	Description	
1	551	100.0	101	2	US-09-033-333-22 Sequence 22, Appl
2	551	100.0	101	2	US-09-033-428-23 Sequence 23, Appl
3	551	100.0	101	2	US-09-033-556-10 Sequence 10, Appl
4	551	100.0	101	2	US-09-614-495-22 Sequence 22, Appl
5	551	100.0	101	2	US-09-898-883-23 Sequence 23, Appl
6	551	100.0	101	2	US-09-151-376-11 Sequence 11, Appl
7	551	100.0	101	2	US-09-814-351-18 Sequence 18, Appl
8	551	100.0	101	2	US-09-814-292-4 Sequence 4, Appl
9	551	100.0	101	2	US-09-814-357-18 Sequence 18, Appl
10	551	100.0	101	2	US-09-875-228-5 Sequence 5, Appl
11	522	94.7	95	2	US-09-392-822A-8 Sequence 8, Appl
12	74	13.4	522	2	US-09-549-519-33 Sequence 33, Appl
13	73.5	13.3	521	2	US-09-489-039A-9549 Sequence 9549, Ap
14	71	12.9	239	2	US-09-934-289A-44 Sequence 44, Appl
15	71	12.9	277	2	US-09-934-289A-42 Sequence 42, Appl
16	71	12.9	283	2	US-08-509-024-2 Sequence 2, Appl
17	71	12.9	283	2	US-09-333-279-2 Sequence 2, Appl
18	71	12.9	283	2	US-09-072-993C-2 Sequence 2, Appl
19	71	12.9	283	2	US-09-631-780-2 Sequence 13, Appl
20	71	12.9	283	2	US-09-334-289A-13 Sequence 13, Appl
21	71	12.9	283	4	PCT-US96-12374-2 Sequence 2, Appl
22	71	12.9	284	2	US-09-949-016-7971 Sequence 7971, Ap
23	70	12.7	406	2	US-09-489-039A-8267 Sequence 8267, Ap
24	70	12.7	749	1	US-08-937-931-8 Sequence 8, Appl
25	70	12.7	749	2	US-09-285-502-8 Sequence 8, Appl
26	70	12.7	749	2	US-09-709-126-8 Sequence 8, Appl
27	70	12.7	749	2	US-09-871-385A-8 Sequence 8, Appl

28 67 12.2 401 2 US-09-489-039A-13241 Sequence 13241, A  
29 67 12.2 491 2 US-09-030-335-2 Sequence 2, Appl  
30 67 12.2 523 2 US-09-549-519-36 Sequence 36, Appl  
31 67 12.2 748 1 US-08-920-234-2 Sequence 2, Appl  
32 67 12.2 748 1 US-08-937-931-4 Sequence 4, Appl  
33 67 12.2 748 2 US-09-285-502-4 Sequence 4, Appl  
34 67 12.2 748 2 US-09-030-335-9 Sequence 9, Appl  
35 67 12.2 748 2 US-09-709-126-4 Sequence 4, Appl  
36 67 12.2 748 2 US-09-871-385A-4 Sequence 4, Appl  
37 67 12.2 761 2 US-09-949-016-10631 Sequence 10631, A  
38 67 12.2 799 2 US-09-030-335-4 Sequence 4, Appl  
39 66.5 12.1 288 2 US-09-248-796A-14840 Sequence 14840, A  
40 66.5 12.1 868 1 US-08-374-834-1 Sequence 1, Appl  
41 66.5 12.1 868 1 US-08-644-271-1 Sequence 1, Appl  
42 66.5 12.1 868 2 US-09-077-955-1 Sequence 1, Appl  
43 66.5 12.1 868 2 US-10-016-283-1 Sequence 1, Appl  
44 66 12.0 184 2 US-09-134-000C-3820 Sequence 3820, Ap  
45 66 12.0 220 2 US-09-328-714A-4 Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-09-033-333-22  
; Sequence 22, Application US/09033333  
; Patent No. 6197293  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De Chao  
; APPLICANT: Schuur, Eric  
; APPLICANT: Henderson, Daniel  
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC  
; TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/033,333  
; FILING DATE: 02-MAR-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Catherine, Polizzi M  
; REGISTRATION NUMBER: 40,130  
; REFERENCE/DOCKET NUMBER: 34802-20007.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 101 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-033-333-22

Query Match 100.0%; Score 551; DB 2; Length 101;

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Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101
Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101

RESULT 2
US-09-033-428-23
; Sequence 23, Application US/09033428
; Patent No. 6254862
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-033-428-23

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101
Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101

RESULT 3
US-09-033-556-10
; Sequence 10, Application US/09033556
; Patent No. 6432700

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; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-09-033-556-10

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 6.9e-60;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60

QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101
Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRDLGKPCSLLLQYD 101

RESULT 4
US-09-614-495-22
; Sequence 22, Application US/09614495
; Patent No. 6436394
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto

```

STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/614,495  
FILING DATE: 11-Jul-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/033,333  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Catherine, Polizzi M  
REGISTRATION NUMBER: 40,130  
REFERENCE/DOCKET NUMBER: 34802-20007.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 101 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-614-495-22

Query Match 100.0%; Score 551; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6.9e-60;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 CLKRRARPPIYRPIIVLPHNEKIHRLDGLKPCSLLOYD 101  
DB 61 CLKRRARPPIYRPIIVLPHNEKIHRLDGLKPCSLLOYD 101

RESULT 5  
US-09-898-883-23  
Sequence 23, Application US/09898883  
Patent No. 6585968  
GENERAL INFORMATION:  
APPLICANT: Little, Andrew  
Lampareki, Henry  
Schuur, Eric  
Henderson, Daniel

TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS  
EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MORRISON & FOERSTER  
STREET: 755 PAGE MILL ROAD  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,883

FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/033,428  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: POLIZZI, CATHERINE M.  
REGISTRATION NUMBER: 40,130  
REFERENCE/DOCKET NUMBER: 34802-30004.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 101 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-898-883-23

Query Match 100.0%; Score 551; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6.9e-60;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSALMFVCLIIIMWLIC 60  
QY 61 CLKRRARPPIYRPIIVLPHNEKIHRLDGLKPCSLLOYD 101  
DB 61 CLKRRARPPIYRPIIVLPHNEKIHRLDGLKPCSLLOYD 101

RESULT 6  
US-09-151-376-11  
Sequence 11, Application US/09151376  
Patent No. 6676935  
GENERAL INFORMATION:  
APPLICANT: Henderson, D.R.  
APPLICANT: Schuur, B.R.  
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS  
FILE REFERENCE: 34802000221  
CURRENT APPLICATION NUMBER: US/09/151,376  
CURRENT FILING DATE: 1998-09-10  
EARLIER APPLICATION NUMBER: 08/669,753  
EARLIER FILING DATE: 1996-06-26  
EARLIER APPLICATION NUMBER: 08/495,034  
EARLIER FILING DATE: 1995-06-27  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 11  
LENGTH: 101  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-151-376-11

Query Match 100.0%; Score 551; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 6.9e-60;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSALMFVCLIIIMWLIC 60  
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DB 61 CLKRRARPPIYRPIIVLPHNEKIHRLDGLKPCSLLOYD 101

RESULT 7  
US-09-814-351-18

; Sequence 18, Application US/09814351  
; Patent No. 6692736

; GENERAL INFORMATION:

; APPLICANT: Yu, De-Chao

; APPLICANT: Li, Yuanhao

; APPLICANT: Henderson, Daniel R.

; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS

; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE

; FILE REFERENCE: 348022001700

; CURRENT APPLICATION NUMBER: US/09/814,351

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/192,156

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence for ADP

US-09-814-351-18

Query Match 100.0%; Score 551; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 8

US-09-814-292-4

; Sequence 4, Application US/09814292

; Patent No. 6852528

; GENERAL INFORMATION:

; APPLICANT: Zhang, Hong

; APPLICANT: Yu, De-Chao

; APPLICANT: Henderson, Daniel R.

; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN

; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING

; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 348022001500

; CURRENT APPLICATION NUMBER: US/09/814,292

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/191,861

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence for ADP

US-09-814-292-4

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Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

Db 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 9

US-09-814-357-18

; Sequence 18, Application US/09814357

; Patent No. 6911200

; GENERAL INFORMATION:

; APPLICANT: Yu, De-Chao

; APPLICANT: Chen, Yu

; APPLICANT: Henderson, Daniel R.

; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA

; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,

; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION

; FILE REFERENCE: 348022001600

; CURRENT APPLICATION NUMBER: US/09/814,357

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 60/192,015

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 18

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Amino acid sequence for ADP

US-09-814-357-18

Query Match 100.0%; Score 551; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 10

US-09-875-228-5

; Sequence 5, Application US/09875228

; Patent No. 6916918

; GENERAL INFORMATION:

; APPLICANT: Yu, D.

; APPLICANT: Henderson, D.R.

; APPLICANT: Schuur, E.R.

; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE

; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF

; FILE REFERENCE: 348022000900

; CURRENT APPLICATION NUMBER: US/09/875,228

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 09/127,834

; PRIOR FILING DATE: 1998-08-03

; PRIOR APPLICATION NUMBER: 60/076,545

; PRIOR FILING DATE: 1998-03-02

; PRIOR APPLICATION NUMBER: 60/054,523

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 5

; LENGTH: 101

; TYPE: PRT

; ORGANISM: Adenovirus

US-09-875-228-5

Query Match 100.0%; Score 551; DB 2; Length 101;

Best Local Similarity 100.0%; Pred. No. 6.9e-60;

Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTGSTTAPTDTYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSTALMFVCLIIIMWLIC 60
Db 1 MTGSTTAPTDTYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSTALMFVCLIIIMWLIC 60
QY 61 CLKRRRARPPYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRARPPYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 11
US-09-392-822A-8
; Sequence 8, Application US/09392822A
; Patent No. 6900049
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: Adenovirus Vectors Containing Cell
; TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
; FILE REFERENCE: CELL-014: 122.1
; CURRENT APPLICATION NUMBER: US/09/392,822A
; CURRENT FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/099,791
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/392,822
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-392-822A-8

Query Match 94.7%; Score 522; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 2.3e-56;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSTALMFVCLIIIMWLICLKRRR 66
Db 1 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSTALMFVCLIIIMWLICLKRRR 60
QY 67 ARPPYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
Db 61 ARPPYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 95

RESULT 12
US-09-549-519-33
; Sequence 33, Application US/09549519
; Patent No. 6673601
; GENERAL INFORMATION:
; APPLICANT: TORDO, NOEL
; APPLICANT: PERRIN, PIERRE
; APPLICANT: JACOB, YVES
; APPLICANT: BAHLOUL, CHOKRI
; TITLE OF INVENTION: CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 03495-0188-00000
; CURRENT APPLICATION NUMBER: US/09/549,519
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,501
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Lyssavirus sp.
; FEATURE:
; OTHER INFORMATION: Laginga
US-09-549-519-33

Query Match 13.4%; Score 74; DB 2; Length 522;
Best Local Similarity 35.0%; Pred. No. 1.5;
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Matches 21; Conservative 8; Mismatches 19; Indels 12; Gaps 3;
QY 24 LNLPOVHAFVNDWASLDMM---WFSIALM-----FVCLIIIMWLICLKRRRARPPYRPP 74
Db 437 VHMPDVHKLVS---VDLGLPWSLYALIGATIIAIFILICIRICCKKGRNSPTNRP 493

RESULT 13
US-09-489-039A-9549
; Sequence 9549, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9549
; LENGTH: 521
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9549

Query Match 13.3%; Score 73.5; DB 2; Length 521;
Best Local Similarity 30.4%; Pred. No. 1.7;
Matches 31; Conservative 16; Mismatches 32; Indels 23; Gaps 8;

QY 4 STIAPTDTYRNTTATGTSALNLPQVHAFVND-----WASL-DMMWFSI-----ALMFVC 52
Db 171 SEVAPTE--MRGKLTGLNEVAIVIGLAAFAINAIIGIINGHLDPVWRYMLLVQAIPAIC 228
QY 53 LIH-MWLICLKRRRARPPYRPIIIVLNPNEKIHRLDGLKP 93
Db 229 LPVGMW-----RA-PESPRWLISKNRHRDEALHILKQIRP 261

RESULT 14
US-09-934-289A-44
; Sequence 44, Application US/09934289A
; Patent No. 6852837
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MBIO98-061CPCIN1(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-289A-44

Query Match 12.9%; Score 71; DB 2; Length 239;
Best Local Similarity 35.9%; Pred. No. 1.3;
Matches 14; Conservative 10; Mismatches 11; Indels 4; Gaps 2;

QY 41 MMWF-----SIALMFVCLIIIMWLICLKRRRARPPYRPII 76
Db 164 VMWFLSGSLVIVIVCSTV-GLIICVKRRKRGDVKVIV 201
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RESULT 15
US-09-934-289A-42
; Sequence 42, Application US/09934289A
; Patent No. 6852837
; GENERAL INFORMATION:
; APPLICANT: Buefield, Samantha J.
; TITLE OF INVENTION: NOVEL MOLECULES OF THE
; TITLE OF INVENTION: HERPESVIRUS-ENTRY-MEDIATOR-RELATED
; TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
; FILE REFERENCE: MEIO98-061CPCNI(M)
; CURRENT APPLICATION NUMBER: US/09/934,289A
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/342,767
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/146,950
; PRIOR FILING DATE: 1998-09-03
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(38)
US-09-934-289A-42

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Query Match      12.9%; Score 71; DB 2; Length 277;
Best Local Similarity 35.9%; Pred. No. 1.6;
Matches 14; Conservative 10; Mismatches 11; Indels 4; Gaps 2;

Qy      41 MWVF--SIALMFVCLIMMLICLKERRARPPYREII 76
Db      202 VMWFLSGSLVIVVCSTV-GLIICVKRRKRGDVVKVIV 239
          :|||  |::|||  :|||::|||  :::|:

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Search completed: January 18, 2006, 19:48:54  
Job time : 23 secs



Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	551	100.0	101	3	US-09-392-822-9	Sequence 9, Appli
2	551	100.0	101	3	US-09-814-292-4	Sequence 4, Appli
3	551	100.0	101	3	US-09-875-228-5	Sequence 5, Appli
4	551	100.0	101	3	US-09-898-883-23	Sequence 23, Appl
5	551	100.0	101	3	US-09-151-376-11	Sequence 11, Appl
6	551	100.0	101	3	US-09-814-357-18	Sequence 18, Appl
7	551	100.0	101	3	US-09-814-351-18	Sequence 18, Appl
8	551	100.0	101	4	US-10-045-116-20	Sequence 20, Appl
9	551	100.0	101	4	US-10-222-479-22	Sequence 22, Appl
10	551	100.0	101	4	US-10-139-089-11	Sequence 11, Appl
11	551	100.0	101	4	US-10-691-045-18	Sequence 18, Appl
12	551	100.0	101	5	US-10-822-873-11	Sequence 11, Appl
13	522	94.7	95	5	US-10-938-227-8	Sequence 8, Appli
14	74	13.4	522	5	US-10-608-538-33	Sequence 33, Appl
15	72	13.1	354	4	US-10-425-115-271104	Sequence 271104,
16	71	12.9	239	3	US-09-934-289A-44	Sequence 44, Appl
17	71	12.9	239	5	US-10-932-991-44	Sequence 44, Appl
18	71	12.9	245	6	US-11-021-951-191	Sequence 191, App
19	71	12.9	277	3	US-09-934-289A-42	Sequence 42, Appl
20	71	12.9	277	4	US-10-369-300-10	Sequence 10, Appl
21	71	12.9	277	5	US-10-932-991-42	Sequence 42, Appl
22	71	12.9	283	3	US-09-924-231-2	Sequence 2, Appli
23	71	12.9	283	3	US-09-934-289A-13	Sequence 13, Appl
24	71	12.9	283	3	US-09-935-727-31	Sequence 31, Appl
25	71	12.9	283	4	US-10-020-787-2	Sequence 2, Appli
26	71	12.9	283	4	US-10-066-209-2	Sequence 2, Appli
27	71	12.9	283	4	US-10-369-300-2	Sequence 2, Appli



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; ORGANISM: Homo sapiens
US-09-151-376-11

Query Match      100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLLIC 60

QY 61 CLKRRRARPPYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 6
US-09-814-357-18
; Sequence 18, Application US/09814357
; Publication No. US2003068307A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-357-18

Query Match      100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLLIC 60

QY 61 CLKRRRARPPYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 7
US-09-814-351-18
; Sequence 18, Application US/09814351
; Publication No. US20030148520A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
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; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-09-814-351-18

Query Match      100.0%; Score 551; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLLIC 60

QY 61 CLKRRRARPPYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 8
US-10-045-116-20
; Sequence 20, Application US/10045116
; Publication No. US20030026792A1
; GENERAL INFORMATION:
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,116
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-045-116-20

Query Match      100.0%; Score 551; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLLIC 60
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Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60  
Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101  
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101

RESULT 9  
US-10-222-479-22  
; Sequence 22, Application US/10222479  
; Publication No. US20030091538A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De Chao  
; Schuur, Eric  
; Henderson, Daniel  
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC  
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS  
; OF USE  
; THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/222,479  
; FILING DATE: 16-Aug-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/614,495  
; FILING DATE: 11-Jul-2000  
; APPLICATION NUMBER: 09/033,333  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Catherine, Polizzi M  
; REGISTRATION NUMBER: 40,130  
; REFERENCE/DOCKET NUMBER: 34802-20007.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 101 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-10-222-479-22

Query Match 100.0%; Score 551; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8.2e-56;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60  
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60  
Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101  
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101

RESULT 11  
US-10-691-045-18  
; Sequence 18, Application US/10691045  
; Publication No. US20040146489A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Li, Yuanhao  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
; COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
; FILE REFERENCE: 348022001700  
; CURRENT APPLICATION NUMBER: US/10/691,045  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US/09/814,351  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/192,156  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18

RESULT 10  
US-10-139-089-11  
; Sequence 11, Application US/10139089  
; Publication No. US20030152553A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, D.R.  
; APPLICANT: Schuur, E.R.  
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS  
; FILE REFERENCE: 348022000221  
; CURRENT APPLICATION NUMBER: US/10/139,089  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 08/669,753  
; PRIOR FILING DATE: 1996-06-26  
; PRIOR APPLICATION NUMBER: 08/495,034  
; PRIOR FILING DATE: 1995-06-27  
; PRIOR APPLICATION NUMBER: 09/509,591  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/151,376  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/033,428  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/039,597  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: 09/033,333  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/039,762  
; PRIOR FILING DATE: 1997-03-03  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 101  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-139-089-11

Query Match 100.0%; Score 551; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 8.2e-56;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60  
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60  
Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101  
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRDLGLKPCSLLLQYD 101

RESULT 11  
US-10-691-045-18  
; Sequence 18, Application US/10691045  
; Publication No. US20040146489A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Li, Yuanhao  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
; COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
; FILE REFERENCE: 348022001700  
; CURRENT APPLICATION NUMBER: US/10/691,045  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: US/09/814,351  
; PRIOR FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/192,156  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18

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; LENGTH: 101
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence for ADP
US-10-691-045-18

Query Match      100.0%; Score 551; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSLMFVCLIIIMWLIC 60
Db 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSLMFVCLIIIMWLIC 60

QY 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101

RESULT 12
US-10-822-873-11
; Sequence 11, Application US/10822873
; Publication No. US20040241857A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, D.R.
; APPLICANT: Schuur, E.R.
; TITLE OF INVENTION: TISSUE SPECIFIC ADENOVIRAL VECTORS
; FILE REFERENCE: CELL-004CON2
; CURRENT APPLICATION NUMBER: US/10/822,873
; CURRENT FILING DATE: 2004-04-13
; PRIOR APPLICATION NUMBER: 09/732,169
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/151,376
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 08/669,753
; PRIOR FILING DATE: 1996-06-26
; PRIOR APPLICATION NUMBER: 08/495,034
; PRIOR FILING DATE: 1995-06-27
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 101
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-873-11

Query Match      100.0%; Score 551; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 8.2e-56;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSLMFVCLIIIMWLIC 60
Db 1 MTGSTAPTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSLMFVCLIIIMWLIC 60

QY 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 CLKRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101

RESULT 13
US-10-938-227-8
; Sequence 8, Application US/10938227
; Publication No. US20050169890A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: Adenovirus Vectors Containing Cell
; FILE REFERENCE: Status-Specific Response Elements and Methods of Use Thereof
; FILE REFERENCE: CELL-014; 122.1
; CURRENT APPLICATION NUMBER: US/10/938,227
; CURRENT FILING DATE: 2004-09-09
; PRIOR APPLICATION NUMBER: 60/099,791
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; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/392,822
; PRIOR FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Adenovirus
US-10-938-227-8

Query Match      94.7%; Score 522; DB 5; Length 95;
Best Local Similarity 100.0%; Pred. No. 1.7e-52;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSLMFVCLIIIMWLICLKRRR 66
Db 1 APTTDYRNTTATGTSALNLPQVHAFVNDWASLDMMWFSLMFVCLIIIMWLICLKRRR 60

QY 67 ARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 101
Db 61 ARPPIYPRIIVLNPNEKIHRLDGLKPCSLLOYD 95

RESULT 14
US-10-608-538-33
; Sequence 33, Application US/10608538
; Publication No. US20050064389A1
; GENERAL INFORMATION:
; APPLICANT: TORDO, NOEL
; APPLICANT: FERRIN, PIERRE
; APPLICANT: JACOB, YVES
; APPLICANT: BAHLOUL, CHOKRI
; TITLE OF INVENTION: CHIMERIC LYSSAVIRUS NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 03495-0188-00000
; CURRENT APPLICATION NUMBER: US/10/608,538
; CURRENT FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: US/09/549,519
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/129,501
; PRIOR FILING DATE: 1999-04-15
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Lyssavirus sp.
; FEATURE:
; OTHER INFORMATION: Lag1NGA
US-10-608-538-33

Query Match      13.4%; Score 74; DB 5; Length 522;
Best Local Similarity 35.0%; Pred. No. 8.7;
Matches 21; Conservative 8; Mismatches 19; Indels 12; Gaps 3;

QY 24 LNLQVHAFVNDWASLDMMWFSLMFVCLIIIMWLICLKRRRARPPIYRP 74
Db 437 VHMPPVHKLVSDDDGLPWSLYALIGATIAFFILICIRICKKRRRNSPTNRP 493

RESULT 15
US-10-425-115-271104
; Sequence 271104, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 271104
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_178843C.1.pep
US-10-425-115-271104

Query Match      13.1%; Score 72; DB 4; Length 354;
Best Local Similarity 26.0%; Pred. No. 9.8;
Matches 27; Conservative 11; Mismatches 34; Indels 32; Gaps 4;

Qy      3 GSTIAPTDTYRNTT-----ATGLTSALNLPQVHAFVNDWASLDMMWFSLALMFVCLIIIM 56
Db      90 GGTAPPEPNSYTFVHIVGDIVALLDALHLPQVVFVGHWDGA-----IVS 134

Qy      57 WLICLKRREARPEIYRPIIVLNPHNEKIHRLDGLKPCSLLLQY 100
Db      135 WNLCLLRPDRV-----ALVNLSVAFMPRRPGVKP-----LEY 167
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Search completed: January 19, 2006, 19:50:07  
Job time : 62 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:46:37 ; Search time 9 Seconds  
(without alignments)  
113.725 Million cell updates/sec

Title: US-10-822-873-11

Perfect score: 551

Sequence: 1 MTGSTIAPTDTYNTATGL.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 70606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_New.\*

- 1: /cgn2\_6/prodata1/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 2: /cgn2\_6/prodata1/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /cgn2\_6/prodata1/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /cgn2\_6/prodata1/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 5: /cgn2\_6/prodata1/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 6: /cgn2\_6/prodata1/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /cgn2\_6/prodata1/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /cgn2\_6/prodata1/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	12.9	283	6	US-10-987-663-4
2	62.5	11.3	222	7	US-11-212-443-174
3	59.5	10.8	222	7	US-11-212-443-175
4	57.5	10.4	1196	6	US-10-613-744-9
5	57	10.3	232	6	US-10-821-234-1199
6	57	10.3	273	6	US-10-353-783-50
7	56	10.2	85	6	US-10-966-648-6
8	56	10.2	103	6	US-10-966-648-27
9	56	10.2	112	7	US-11-139-435-2
10	56	10.2	1191	7	US-11-139-435-2
11	56	10.2	1274	6	US-10-454-437-360
12	55	10.0	113	6	US-10-467-657-5542
13	55	10.0	274	6	US-10-353-783-51
14	55	10.0	593	7	US-11-212-443-64
15	55	10.0	3716	7	US-11-052-554A-141
16	54.5	9.9	269	7	US-11-055-822-510
17	54	9.8	389	6	US-10-467-657-4468
18	54	9.8	717	6	US-10-467-657-8056
19	54	9.8	732	7	US-11-082-389-94
20	54	9.8	772	7	US-11-147-238-2
21	54	9.8	772	7	US-11-147-238-5
22	54	9.8	1150	7	US-11-139-435-1
23	54	9.8	1193	7	US-11-139-435-3
24	53.5	9.7	225	6	US-10-467-657-2276
25	53.5	9.7	468	6	US-10-957-569-28

26	53	9.6	178	6	US-10-521-162-7	Sequence 7, Appli
27	53	9.6	226	7	US-11-148-012-3	Sequence 3, Appli
28	53	9.6	309	7	US-11-165-160-2	Sequence 2, Appli
29	53	9.6	386	7	US-11-055-822-586	Sequence 586, App
30	53	9.6	650	6	US-10-467-657-1948	Sequence 1948, Ap
31	52.5	9.5	226	7	US-11-148-012-2	Sequence 2, Appli
32	52.5	9.5	366	6	US-10-661-426-4	Sequence 4, Appli
33	52.5	9.5	366	6	US-10-661-426-7	Sequence 7, Appli
34	52.5	9.5	366	6	US-10-661-426-13	Sequence 13, Appli
35	52.5	9.5	1304	6	US-10-821-234-1648	Sequence 1648, Ap
36	52	9.4	64	7	US-11-000-463-259	Sequence 259, App
37	52	9.4	187	5	US-09-978-360A-758	Sequence 758, App
38	52	9.4	598	7	US-11-113-837-18	Sequence 18, Appli
39	51.5	9.3	266	6	US-10-353-783-57	Sequence 57, Appli
40	51.5	9.3	557	7	US-11-191-374-4	Sequence 4, Appli
41	51.5	9.3	557	7	US-11-191-375-4	Sequence 4, Appli
42	51.5	9.3	557	7	US-11-191-588-4	Sequence 4, Appli
43	51.5	9.3	801	6	US-10-454-437-278	Sequence 278, App
44	51.5	9.3	801	7	US-11-174-150-29	Sequence 29, Appli
45	51.5	9.3	801	7	US-11-124-368A-292	Sequence 292, Appli

#### ALIGNMENTS

##### RESULT 1

US-10-987-663-4  
; Sequence 4, Application US/10987663  
; Publication No. US20050272118A1  
; GENERAL INFORMATION:  
; APPLICANT: GENENTECH, INC.  
; APPLICANT: CLARK, HILARY  
; APPLICANT: EATON, DANIEL L.  
; APPLICANT: WRANIK, BERND  
; APPLICANT: OUYANG, WENJUN  
; APPLICANT: GONZALES, LINO  
; APPLICANT: LOYET, KELLY M.  
; TITLE OF INVENTION: Novel Compositions and Methods for the Treatment of  
; TITLE OF INVENTION: Immune Related Diseases  
; FILE REFERENCE: P1996R1P1-US  
; CURRENT APPLICATION NUMBER: US/10/987,663  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: US 60/421,236  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: US 10/371,341  
; PRIOR FILING DATE: 2003-02-19  
; NUMBER OF SEQ ID NOS: 10  
; SEQ ID NO 4  
; LENGTH: 283  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-987-663-4

Query Match 12.9%; Score 71; DB 6; Length 283;

Best Local Similarity 35.9%; Pred. No. 0.17;

Matches 14; Conservative 10; Mismatches 11; Indels 4; Gaps 2;

QY 41 MWVF---STALMFVCLIIIMWLICLKRRRRRPPPIVRPII 76

Db 202 VWFLGSLVIVIVCVSTV-GLIICVKRKRPRGVDVKVIV 239

##### RESULT 2

US-11-212-443-174  
; Sequence 174, Application US/11212443  
; Publication No. US20050287165A1  
; GENERAL INFORMATION:  
; APPLICANT: Scalato, Enzo  
; APPLICANT: Masignani, Vega  
; APPLICANT: Rappuoli, Rino  
; APPLICANT: Pizza, Mariagrazia  
; APPLICANT: Grandi, Guido  
; TITLE OF INVENTION: Meningococcal Antigens

```
; FILE REFERENCE: CHIRO159
; CURRENT APPLICATION NUMBER: US/11/212,443
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/09/302,626
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ORF39
;
; NAME/KEY: SITE
; LOCATION: (17)..(33)
; OTHER INFORMATION: place-holder
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (53)..(67)
; OTHER INFORMATION: place-holder
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (211)
; OTHER INFORMATION: place-holder
;
; US-11-212-443-174

Query Match 11.3%; Score 62.5; DB 7; Length 222;
Best Local Similarity 25.3%; Pred. No. 1..4;
Matches 26; Conservative 15; Mismatches 37; Indels 25; Gaps 5;

Qy 3 GSTIAPTD---VRN-TTATGLTSALNLPQVHAFVNDWASLDNWFSIALMFVCLIMWL 58
Db 113 GDTVARRELEQIRNFLTQALTSVLDLAFSFIFL-----AVMWYSSTLTWVVLASLIC 167

Qy 59 ICCLKRRRARPPIVRPIIVLPHNEKIHRLDGLKPCSLLLQYD 101
Db 168 ICA-----NRTVLII-----AHLRSTVKTARIIMD 194

RESULT 3
US-11-212-443-175
; Sequence 175, Application US/11212443
; Publication No. US20050287165A1
; GENERAL INFORMATION:
; APPLICANT: Scalato, Enzo
; APPLICANT: Massignani, Vega
; APPLICANT: Rappuoli, Rino
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Grandi, Guido
; TITLE OF INVENTION: Meningococcal Antigens
; FILE REFERENCE: CHIRO159
; CURRENT APPLICATION NUMBER: US/11/212,443
; CURRENT FILING DATE: 2005-08-24
; PRIOR APPLICATION NUMBER: US/09/302,626
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT/IB99/00103
; PRIOR FILING DATE: 1999-01-14
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 175
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: overlap identity
;
; NAME/KEY: SITE
; LOCATION: (16)..(33)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (53)..(67)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (71)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (79)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (83)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (101)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (104)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (109)
; OTHER INFORMATION: absent or positive
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; NAME/KEY: SITE
; LOCATION: (123)
; OTHER INFORMATION: absent or positive
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; NAME/KEY: SITE
; LOCATION: (137)
; OTHER INFORMATION: absent or positive
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; NAME/KEY: SITE
; LOCATION: (141)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (147)
; OTHER INFORMATION: absent or positive
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; NAME/KEY: SITE
; LOCATION: (155)..(156)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (159)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (163)
; OTHER INFORMATION: absent or positive
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; NAME/KEY: SITE
; LOCATION: (166)
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; LOCATION: (170)
; OTHER INFORMATION: absent or positive
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; LOCATION: (186)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (188)
; OTHER INFORMATION: absent or positive
; FEATURE:
; NAME/KEY: SITE
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/ MEDIUM TYPE: Floppy disk  
/ COMPUTER: IBM PC compatible  
/ OPERATING SYSTEM: PC-DOS/MS-DOS  
/ SOFTWARE: Patentin Release #1.0, Version #1.30  
/ CURRENT APPLICATION DATA:  
/ APPLICATION NUMBER: US/10/353,783  
/ FILING DATE: 28-Jan-2003  
/ CLASSIFICATION: <Unknown>  
/ PRIOR APPLICATION DATA:  
/ APPLICATION NUMBER: 08/448,729  
/ FILING DATE: 24-MAY-1995  
/ APPLICATION NUMBER: 08/172,329  
/ FILING DATE: 21-DEC-1993  
/ APPLICATION NUMBER: 07/982,255  
/ FILING DATE: 25-NOV-1992  
/ APPLICATION NUMBER: 07/684,535  
/ FILING DATE: 10-APR-1991  
/ APPLICATION NUMBER: 07/589,701  
/ FILING DATE: 01-OCT-1990  
/ APPLICATION NUMBER: 07/573,616  
/ FILING DATE: 24-AUG-1990  
/ APPLICATION NUMBER: 07/537,198  
/ FILING DATE: 11-JUN-1990  
/ APPLICATION NUMBER: 07/422,383  
/ FILING DATE: 16-OCT-1989  
/ ATTORNEY/AGENT INFORMATION:  
/ NAME: Clough, David W.  
/ REGISTRATION NUMBER: 36,107  
/ REFERENCE/DOCKET NUMBER: 01017/32958A  
/ TELECOMMUNICATION INFORMATION:  
/ TELEPHONE: 312/474-6300  
/ TELEFAX: 312/474-0448  
/ TELEX: <Unknown>  
/ INFORMATION FOR SEQ ID NO: 50:  
/ SEQUENCE CHARACTERISTICS:  
/ LENGTH: 273 amino acids  
/ TYPE: amino acid  
/ STRANDEDNESS: single  
/ TOPOLOGY: linear  
/ MOLECULE TYPE: protein  
/ SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
US-10-353-783-50

Query Match 10.3%; Score 57; DB 6; Length 273;  
Best Local Similarity 26.0%; Pred.No. 8.3;  
Matches 27; Conservative 18; Mismatches 39; Indels 20; Gaps 5;  
QY 1 MTGSTIAPTDTYRTNTATGTSALNLPQVHA--FVNDWASLD-----MMWFSLA 47  
Db 164 VVSSTLSPEKDSR-----VSVTKPFLPPVAASSLRNDSSSNRKAKNPTGDSLSLHWAAMA 219  
QY 48 L-MFVCLIIIMWLICCLKRRRARRPIYRPI--IVLNPHNEKHRL 89  
Db 220 LPAPFSLIIGFAFGALYWKRPQSLTRAveniQINEEDNEISML 263

RESULT 7  
US-10-966-648-6  
/ Sequence 6, Application US/10966648  
/ Publication No. US20050249734A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sutcliffe, J. Gregor  
/ APPLICANT: de Lecea, Luis  
/ APPLICANT: Henriksen, Steven J.  
/ APPLICANT: Siggins, George R.  
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods  
/ FILE REFERENCE: 14740A-000640US  
/ CURRENT APPLICATION NUMBER: US/10/966,648  
/ CURRENT FILING DATE: 2004-10-14  
/ PRIOR APPLICATION NUMBER: US 08/648,322  
/ PRIOR FILING DATE: 1996-05-15  
/ PRIOR APPLICATION NUMBER: US 08/857,389

/ PRIOR FILING DATE: 1997-05-15  
/ PRIOR APPLICATION NUMBER: US 09/766,396  
/ PRIOR FILING DATE: 2001-01-18  
/ NUMBER OF SEQ ID NOS: 31  
/ SOFTWARE: Patentin Ver. 2.1  
/ SEQ ID NO 6  
/ LENGTH: 85  
/ TYPE: PRT  
/ ORGANISM: Rattus sp.  
/ FEATURE:  
/ OTHER INFORMATION: rat procortistatin  
US-10-966-648-6

Query Match 10.2%; Score 56; DB 6; Length 85;  
Best Local Similarity 36.4%; Pred.No. 3;  
Matches 12; Conservative 5; Mismatches 4; Indels 12; Gaps 2;  
QY 62 LKRRRARRPIYRPIIVLNPHNEKHRLDGLKPC 94  
Db 53 LSKRQRRPPLQOP-----PHRDK-----KPC 73

RESULT 8  
US-10-966-648-27  
/ Sequence 27, Application US/10966648  
/ Publication No. US20050249734A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sutcliffe, J. Gregor  
/ APPLICANT: de Lecea, Luis  
/ APPLICANT: Henriksen, Steven J.  
/ APPLICANT: Siggins, George R.  
/ APPLICANT: The Scripps Research Institute  
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods  
/ FILE REFERENCE: 14740A-000640US  
/ CURRENT APPLICATION NUMBER: US/10/966,648  
/ CURRENT FILING DATE: 2004-10-14  
/ PRIOR APPLICATION NUMBER: US 08/648,322  
/ PRIOR FILING DATE: 1996-05-15  
/ PRIOR APPLICATION NUMBER: US 08/857,389  
/ PRIOR FILING DATE: 1997-05-15  
/ PRIOR APPLICATION NUMBER: US 09/766,396  
/ PRIOR FILING DATE: 2001-01-18  
/ NUMBER OF SEQ ID NOS: 31  
/ SOFTWARE: Patentin Ver. 2.1  
/ SEQ ID NO 27  
/ LENGTH: 103  
/ TYPE: PRT  
/ ORGANISM: Rattus sp.  
/ FEATURE:  
/ OTHER INFORMATION: positions 10-112 of rat preprocortistatin (CST),  
/ OTHER INFORMATION: cortistatin-29  
US-10-966-648-27

Query Match 10.2%; Score 56; DB 6; Length 103;  
Best Local Similarity 36.4%; Pred.No. 3.8;  
Matches 12; Conservative 5; Mismatches 4; Indels 12; Gaps 2;  
QY 62 LKRRRARRPIYRPIIVLNPHNEKHRLDGLKPC 94  
Db 71 LSKRQRRPPLQOP-----PHRDK-----KPC 91

RESULT 9  
US-10-966-648-2  
/ Sequence 2, Application US/10966648  
/ Publication No. US20050249734A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Sutcliffe, J. Gregor  
/ APPLICANT: de Lecea, Luis  
/ APPLICANT: Henriksen, Steven J.  
/ APPLICANT: Siggins, George R.  
/ APPLICANT: The Scripps Research Institute  
/ TITLE OF INVENTION: Antibodies to Cortistatin, Compositions and Methods





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; FILE REFERENCE: 30853/40359A
; CURRENT APPLICATION NUMBER: US/11/052,554A
; CURRENT FILING DATE: 2005-02-07
; PRIOR APPLICATION NUMBER: US 60/589,227
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004
; PRIOR FILING DATE: 2004-02-06
; NUMBER OF SEQ ID NOS: 763
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141
; LENGTH: 3716
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-141

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Query Match      10.0%; Score 55; DB 7; Length 3716;
Best Local Similarity 35.0%; Pred. No. 2.5e+02;
Matches 14; Conservative 5; Mismatches 19; Indels 2; Gaps 1;

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QY      6  IAPTTDYRNTTATGLTSALN--LPQVHAFVNDWASLDMWW 43
Db      2445 VPPTPGFGNTTATPSSGFFNSGAGVSGFGNGVNLGWW 2484

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Search completed: January 18, 2006, 19:50:27  
Job time : 9 secs

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## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**

**This Page Blank (uspto)**



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OM protein - protein search, using sw model

Run on: January 18, 2006, 19:42:41 ; Search time 70 Seconds  
(without alignments)  
1017.977 Million cell updates/sec

Title: US-10-822-873-11  
Perfect score: 551  
Sequence: 1 MTGSTIAPTDTYRNTATG.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 05.80.\*  
1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	551	100.0	101	1	E311_ADE02	P24935 human adeno
2	551	100.0	101	2	Q779E8_ADE02	Q779E8 human adeno
3	548	99.5	101	2	Q910Z3_ADE02	Q910Z3 human adeno
4	545	98.9	101	2	Q912J6_ADE02	Q912J6 human adeno
5	538	97.6	101	1	E311_ADE06	O55653 human adeno
6	355	64.4	94	2	O12392_ADE01	O12392 human adeno
7	346	62.8	93	1	E311_ADE05	P17590 human adeno
8	346	62.8	93	2	Q6VGT8_ADE08	Q6VGT8 human adeno
9	107.5	19.5	276	2	Q76C86_ADE08	Q76C86 human adeno
10	107.5	19.5	276	2	Q80IV7_ADE08	Q80IV7 human adeno
11	102.5	18.6	296	2	Q5TIZ2_ADE09	Q5TIZ2 human adeno
12	101	18.3	261	2	Q76EL5_ADE08	Q76EL5 human adeno
13	100.5	18.2	281	2	Q4KS19_ADE08	Q4KS19 human adeno
14	90.5	16.4	259	2	Q7TBG9_ADE08	Q7TBG9 human adeno
15	77	14.0	235	2	Q90770_CHICK	Q90770 gallus gall
16	77	14.0	235	2	Q6RI33_CHICK	Q6RI33 gallus gall
17	77	14.0	235	2	Q6QR65_CHICK	Q6QR65 gallus gall
18	77	14.0	235	2	Q6QR63_CHICK	Q6QR63 gallus gall
19	76.5	13.9	435	2	Q4PET9_USTMA	Q4PET9 ustilago ma
20	76.5	13.9	866	2	Q6CQI7_KLUJA	Q6CQI7 kluyveromyc
21	76	13.8	235	2	Q6QR62_CHICK	Q6QR62 gallus gall
22	76	13.8	235	2	Q6QR64_CHICK	Q6QR64 gallus gall
23	75.5	13.7	503	2	Q84O68_ORYSA	Q84O68 oryza sativ
24	74.5	13.5	163	2	Q87602_SIVCZ	Q87602 chimpanzee
25	74	13.4	283	2	Q9XSZ8_CERAE	Q9XSZ8 cercopithec
26	74	13.4	522	2	Q91C27_9RHAB	Q91C27 lagos bat v
27	74	13.4	544	1	ADA10_RAT	Q10743 rattus norv
28	73.5	13.3	347	2	Q88TH9_LACPL	Q88TH9 lactobacill
29	73.5	13.3	1070	2	Q5KDV0_CRYNE	Q5KDV0 cryptococcu
30	72	13.1	92	2	Q5C818_SCHJA	Q5C818 schistosoma
31	72	13.1	128	2	Q5C807_SCHJA	Q5C807 schistosoma

RESULT 1										
E311_ADE02	ID	E311_ADE02	STANDARD;	PRT;	101 AA.					
AC	P24975;									
DT	01-MAR-1992	(Rel. 21, Created)								
DT	01-MAR-1992	(Rel. 21, Last sequence update)								
DT	10-MAY-2005	(Rel. 47, Last annotation update)								
DE	Early E3A 11.6 kDa glycoprotein.									
OS	Human adenovirus 2 (HAdV-2).									
OC	Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.									
OX	NCBI_TaxID=10515;									
RN	[1]									
RP	NUCLEOTIDE SEQUENCE.									
RX	MEDLINE=81053687; PubMed=6253880;									
RA	Herisse J., Courtois G., Galibert F.;									
RT	"Nucleotide sequence of the EcoRI D fragment of adenovirus 2 genome.";									
RL	Nucleic Acids Res. 8:2173-2192(1980).									
RN	[2]									
RP	IDENTIFICATION OF PROTEIN.									
RX	MEDLINE=93079877; PubMed=1448922;									
RA	Scaria A., Tollefson A.E., Saha S.K., Wold W.S.M.;									
RT	"The E3-11.6K protein of adenovirus is an Asn-glycosylated integral									
RT	membrane protein that localizes to the nuclear membrane.";									
RL	Virology 191:743-753(1992).									
CC	-!- SUBCELLULAR LOCATION: Integral nuclear membrane protein.									
CC	-!- PTM: N-glycosylated and probably also O-glycosylated.									
CC	-!- SIMILARITY: Belongs to the adenoviruses E3A-1 family.									
CC	-----									
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration									
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -									
CC	the European Bioinformatics Institute. There are no restrictions on its									
CC	use as long as its content is in no way modified and this statement is not									
CC	removed.									
CC	-----									
EMBL	J01917; AAA92222.1; -; Genomic_DNA.									
DR	InterPro; IPR008652; Hum_adeno_E3A.									
DR	Pfam; PF05393; Hum_adeno_E3A; 1.									
DR	Early protein; Glycoprotein; Transmembrane.									
FT	TRANSMEM 41 62 Potential.									
FT	CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).									
SQ	SEQUENCE 101 AA; 11644 MW; FB89FCC6E921E84B CRC64;									
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Query Match		100.0%;		Score 551;		DB 1;		Length 101;		
Best Local Similarity		100.0%;		Pred. No. 1e-52;						
Matches 101;		Conservative 0;		Mismatches 0;		Indels 0;		Gaps 0;		
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Qy	1	MTGSTIAPTDTYRNTATG	1	TSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLC	60					
Db	1	MTGSTIAPTDTYRNTATG	1	TSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLC	60					
Qy	61	CLKRRRARPPIYRPIIVLNP	61	HNPKIHRDLGLKPCSLLLQYD	101					
Db	61	CLKRRRARPPIYRPIIVLNP	61	HNPKIHRDLGLKPCSLLLQYD	101					

```
RESULT 2
Q779E8_ADE02
ID Q779E8_ADE02 PRELIMINARY; PRT; 101 AA.
AC Q779E8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE 11.6K protein.
OS Human adenovirus 2 (HAdV-2).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ear swab, Respiratory epithelium, and stool sample;
RA Borchering F., Pring-Akerblom P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293914; CAC67713.1; -; Genomic DNA.
DR EMBL; AJ293916; CAC67729.1; -; Genomic DNA.
DR EMBL; AJ293917; CAC67737.1; -; Genomic DNA.
DR EMBL; AJ293912; CAC67696.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
SQ SEQUENCE 101 AA; 11644 MW; F899FCC6E921E84B CRC64;

Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1e-52;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
DB 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60

QY 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 3
Q910Z3_ADE02
ID Q910Z3_ADE02 PRELIMINARY; PRT; 101 AA.
AC Q910Z3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 11.6K protein.
OS Human adenovirus 2 (HAdV-2).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liquor;
RA Borchering F., Pring-Akerblom P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293915; CAC67721.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
SQ SEQUENCE 101 AA; 11662 MW; 914F50AC2F8B284F CRC64;

Query Match 99.58; Score 548; DB 2; Length 101;
Best Local Similarity 99.08; Pred. No. 2.2e-52;
Matches 100; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
DB 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60

QY 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 4
Q912J6_ADE02
ID Q912J6_ADE02 PRELIMINARY; PRT; 101 AA.
AC Q912J6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 11.6K protein.
OS Human adenovirus 2 (HAdV-2).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10515;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Borchering F., Pring-Akerblom P.;
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ293913; CAC67704.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
SQ SEQUENCE 101 AA; 11704 MW; E13857DC5891E85B CRC64;

Query Match 98.9%; Score 545; DB 2; Length 101;
Best Local Similarity 99.0%; Pred. No. 4.8e-52;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60
DB 1 MTGSTTAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLLIIMWLIC 60

QY 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPIYPRIIVLNPNEKIHRLDGLKPCSLLLQYD 101

RESULT 5
E311_ADE06
ID E311_ADE06 STANDARD; PRT; 101 AA.
AC O55653;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Early E3A 11.6 kDa glycoprotein.
OS Human adenovirus 6 (HAdV-6).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10534;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA Reichmann H., Schaarschmidt E., Geisler B., Hausmann J., Ortmann D.,
RA Bauer U., Flunker G., Seidel W.;
RT "Sequence analysis of group C human adenoviruses type 1 and 6 for five
genes of region E3."
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral nuclear membrane protein.
CC -1- PTM: N-glycosylated and probably also O-glycosylated (by
similarity).
CC -1- SIMILARITY: Belongs to the adenoviruses E3A-1 family.
CC
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removed.
CC
CC EMBL; Y16037; CAA75991.1; -; Genomic DNA.
DR InterPro; IPR008652; Hum adeno E3A.
DR PFam; PF05393; Hum adeno E3A; 1.
KW Early protein; Glycoprotein; Transmembrane.
TRANSMEM 41 62
FT TRANSMEM 14 14 N-linked (GLCNAC...) (Potential).
FT CBOHYD 101 AA; 11613 MW; EF219000939E3B4B CRC64;
SQ SEQUENCE 101 AA; 11613 MW; EF219000939E3B4B CRC64;
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Query Match          97.6%; Score 538; DB 1; Length 101;
Best Local Similarity 98.0%; Pred. No. 2.8e-51;
Matches 99; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTGSIATPTDYRTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60
DB 1 MTGSIATPTDYRTATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60

QY 61 CLKRRRPPPIYRPIIVLPHNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRPPPIYRPIIVLPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 6
O12392_ADR01
ID O12392_ADE01 PRELIMINARY; PRT; 94 AA.
AC O12392;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE 11.6K protein (10.7 kDa protein).
GN Names:Adi/E3-11.6K;
OS Human adenovirus 1 (HAdV-1).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN:Hannover /Adrian German reference center for adenoviruses;
RA Reichmann H., Schaarschmidt E., Geisler B., Hausmann J., Ortmann D.,
RA Bauer U., Flunker G., Seidel W.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN:Hannover /Adrian German reference center for adenoviruses;
RA Reichmann H., Schaarschmidt E.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15302955; DOI=10.1099/vir.0.80118-0;
RA Lauer K.P., Llorente I., Blair E., Sato J., Kraenov V.,
RA Purkayastha A., Ditty S.E., Hadfield T.L., Buck C., Tibbetts C.,
RA Seto D.;
RT "Natural variation among human adenoviruses: genome sequence and
RT annotation of human adenovirus serotype 1.";
RL J. Gen. Virol. 85:2615-2625(2004).
DR EMBL; Y11257; CAA72127.1; -; Genomic DNA.
DR EMBL; Y11032; CAA71916.1; -; Genomic DNA.
DR EMBL; AF534906; AAQ10560.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum_adeno_E3A; I.
DR Pfam; PF05393; Hum_adeno_E3A; I.
SQ SEQUENCE 94 AA; 10674 MW; D1148B5AFE771862 CRC64;

Query Match          64.4%; Score 355; DB 2; Length 94;
Best Local Similarity 78.8%; Pred. No. 3.8e-31;
Matches 63; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 16 TATGTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLCCKRRRPPPIYRPI 75
DB 10 TATGLTSTQDMPQVSTFVNWNANLGMWFSIALMFVCLIIIMWLSCLCKRRRPPPIYKPI 69

QY 76 IVLPHNEKIHRLDGLKPC 95
DB 70 IVLPHNEKIHRLDGLKPC 89

RESULT 7
E311_ADE05
ID E311_ADR05 STANDARD; PRT; 93 AA.
AC P17590;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
```

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DE Early E3A 10.5 kDa glycoprotein.
OS Human adenovirus 5 (HAdV-5).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=28285;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=2981456;
RA Cladaras C., Wold W.S.M.;
RL "DNA sequence of the early E3 transcription unit of adenovirus 5.";
RT Virology 140:28-43(1985).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=92087470; PubMed=1727603;
RA Chroboczek J., Bieber F., Jacrot B.;
RT "The sequence of the genome of adenovirus type 5 and its comparison
RT with the genome of adenovirus type 2.";
RL Virology 186:280-285(1992).
CC 1- SUBCELLULAR LOCATION: Integral nuclear membrane protein.
CC 1- PTM: N-glycosylated and probably also O-glycosylated.
CC 1- SIMILARITY: Belongs to the adenoviruses E3A-1 family.
CC -----
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CC removed.
CC -----
DR EMBL; M73260; -; NOT ANNOTATED_CDS; Genomic_DNA.
DR EMBL; X03002; CAA36784.1; -; Genomic_DNA.
DR PIR; A05245; ERA53.
DR InterPro; IPR008652; Hum_adeno_E3A.
DR Pfam; PF05393; Hum_adeno_E3A; I.
KW Early protein; Glycoprotein; Transmembrane.
FT TRANSMEM 34 55 Potential.
FT CARBOHYD 3 3 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 93 AA; 10523 MW; 008AD087AAB45A8F CRC64;

Query Match          62.8%; Score 346; DB 1; Length 93;
Best Local Similarity 78.3%; Pred. No. 3.7e-30;
Matches 65; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 14 NTT-----ATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLCCKRRRARP 69
DB 3 NTTNAAATGLTSTNTPTQVSAPVNNWNLGMWFSIALMFVCLIIIMWLCCKRRARP 62

QY 70 PIYRPIIVLPHNEKIHRLDGLK 92
DB 63 PIYSPPIVLPNNNGIHRLDGLK 85

RESULT 8
Q6VGT8_9ADEN
ID Q6VGT8_9ADEN PRELIMINARY; PRT; 93 AA.
AC Q6VGT8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E3 10.5K.
OS Human adenovirus C.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=129951;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA McAllister D.L., Lu F., Thomas B.K., Hutchins B.M., Sugarman B.J.;
RT "Complete Nucleic Acid Sequence of the Adenovirus Type 5 Reference
RT Material.";
RL Bioprocessing 0:0-0(2003).
DR EMBL; AY339865; AAQ19306.1; -; Genomic DNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR008652; Hum_adeno_E3A.
DR Pfam; PF05393; Hum_adeno_E3A; I.
SQ SEQUENCE 93 AA; 10523 MW; 008AD087AAB45A8F CRC64;
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Query Match 62.8%; Score 346; DB 2; Length 93;
Best Local Similarity 78.3%; Pred. No. 3.7e-30;
Matches 65; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

QY 14 NTT-----ATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLICLKRARP 69
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 3 NTTNAAAATGLTSTTTPQVSAFVNNWDLGMWFSIALMFVCLIIIMWLICLKRARP 62

QY 70 PIYRPIIVLNPHEKTHRLDGLK 92
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 PIYSPIIIVLHPNNDGIHRLDGLK 85

RESULT 9
Q76C86_ADE08 PRELIMINARY; PRT; 276 AA.
AC Q76C86;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE E3B1-2 30.8k.
OS Human adenovirus 8 (HAdV-8).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=31545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=8p prime; DOI=10.1136/jcp.56.2.120;
RX PubMed=12560390;
RA Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
RA Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukoyama A., Matsuno S.,
RA Inada T., Okabe N.;
RT "Genetic Characterization of Adenovirus type 8 Isolated in Hiroshima
RT City over a 15-year Period.";
RL J. Clin. Pathol. 56:120-125(2003).
DR EMBL; AB110079; BAC82700.1; -; Genomic DNA.
SQ SEQUENCE 276 AA; 30879 MW; 838596E7F65BEE CRC64;

Query Match 19.5%; Score 107.5; DB 2; Length 276;
Best Local Similarity 28.8%; Pred. No. 0.0021;
Matches 23; Conservative 21; Mismatches 23; Indels 13; Gaps 3;

QY 9 TTDYRNTTATGLTSALNLPQVHAFVND-----WASLD--MMWFSIALMFVCLIIIM 56
   ||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 176 TTDQTEATSSAFSSTANLTSL-ASVNETIVPMYGPYSGLDIQITFLVVGIFILVLL 234

QY 57 WLICLKRARRRPPYRPPII 76
   :||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 235 YFVCKKAREKSRPIYRPVI 254

RESULT 10
Q80I17_ADE08 PRELIMINARY; PRT; 276 AA.
AC Q80I17;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE A5 protein.
OS Human adenovirus type 8E.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=216370;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=99SRU29552;
RX PubMed=12560390; DOI=10.1136/jcp.56.2.120;
RA Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
RA Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukoyama A., Matsuno S.,
RA Inada T., Okabe N.;
RT "Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
RT City over a 15-year Period.";
RL J. Clin. Pathol. 56:120-125(2003).
DR EMBL; AB097769; BAC58004.1; -; Genomic DNA.
SQ SEQUENCE 276 AA; 30919 MW; 587D4C95AE86BC26 CRC64;

Query Match 19.5%; Score 107.5; DB 2; Length 276;
Best Local Similarity 28.8%; Pred. No. 0.0021;
Matches 23; Conservative 21; Mismatches 23; Indels 13; Gaps 3;

QY 9 TTDYRNTTATGLTSALNLPQVHAFVND-----WASLD--MMWFSIALMFVCLIIIM 56
   ||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 176 TTDQTEATSSAFSSTANLTSL-ASVNETIVPMYGPYSGLDIQITFLVVGIFILVLL 234

QY 57 WLICLKRARRRPPYRPPII 76
   :||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 235 YFVCKKAREKSRPIYRPVI 254

RESULT 11
Q5TIZ2_ADE09 PRELIMINARY; PRT; 296 AA.
AC Q5TIZ2;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE E3 orf3 33.1 kDa protein.
GN Name=E3 33.1 k;
OS Human adenovirus 9 (HAdV-9).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=10527;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=type strain: ATCC VR-1086;
RA Buettner W.H., Veres-Molnar S.K.;
RT "Adenovirus type 9, complete sequence.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ854486; CA105981.1; -; Genomic DNA.
SQ SEQUENCE 296 AA; 33125 MW; 256ED64914353439 CRC64;

Query Match 18.6%; Score 102.5; DB 2; Length 296;
Best Local Similarity 26.2%; Pred. No. 0.0079;
Matches 21; Conservative 23; Mismatches 23; Indels 13; Gaps 3;

QY 9 TTDYRNTTATGLTSALNLPQVHAFVND-----WASLD--MMWFSIALMFVCLIIIM 56
   ||||| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::| ::::|
Db 196 TTEQTEATSSAFSSTANLTSL-AWTNETGVSMLHGQPYSGLDIQITFLVVGIFILVLL 254

QY 57 WLICLKRARRRPPYRPPII 76
   :||| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
Db 255 YFVCKKAREKSRPIYRPVI 274

RESULT 12
Q76EL5_ADE08 PRELIMINARY; PRT; 261 AA.
AC Q76EL5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE E3A5 20.3k.
OS Human adenovirus 8 (HAdV-8).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=31545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=130H;
RX PubMed=12560390; DOI=10.1136/jcp.56.2.120;
RA Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
RA Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukoyama A., Matsuno S.,
RA Inada T., Okabe N.;
RT "Genetic Characterization of Adenovirus type 8 Isolated in Hiroshima
RT City over a 15-year Period.";
RL J. Clin. Pathol. 56:120-125(2003).
DR EMBL; AB106356; BAC87854.1; -; Genomic DNA.
SQ SEQUENCE 261 AA; 29415 MW; 91433010DAA30680 CRC64;

Query Match 18.3%; Score 101; DB 2; Length 261;
```

```

Best Local Similarity   24.0%; Pred. No. 0.01;
Matches 18; Conservative 23; Mismatches 34; Indels 0; Gaps 0;

Qy 2 TGSTIAPTDTYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSTALMFVCLIMFWLIC 61
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 165 TDATLSAFSSSTANLTSMTWTGVLMLHGQPYSGLHIQTIFLVICGIFILWLLYFVCC 224
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 62 LKRRARPPIYRPVI 76
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 225 KARKKSRRPIYRPVI 239
    ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
ID Q4KS19_9ADEN PRELIMINARY; PRT; 281 AA.
AC Q4KS19;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE 281k.
OS Human adenovirus type 46.
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=46941;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Police S.R.;
RT "Genome Sequence of Human adenovirus type 46."
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY875648; AAX70939.1; -; Genomic DNA.
SQ SEQUENCE 281 AA; 30918 MW; 23CFB1230DA2032 CRC64;

Query Match      18.2%; Score 100.5; DB 2; Length 281;
Best Local Similarity 26.2%; Pred. No. 0.012;
Matches 21; Conservative 22; Mismatches 24; Indels 13; Gaps 3;

Qy 9 TTDYRNTTATGLTSALNLPQVHAFVND-----WASLD--MWFSIALMFVCLIIIM 56
    ||:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 181 TTEQTEATSSAFSSSTANTSL-AWNTETGVSLMNRQPSGLDIQTIFLVVCGIFILAVLL 239
    |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 57 WLICLCERRARRPPIYRPVI 76
    |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 240 YFVCCKAREKSRRPIYRPVI 259
    |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 14
Q7TBG9_ADE08
ID Q7TBG9_ADE08 PRELIMINARY; PRT; 259 AA.
AC Q7TBG9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E3B1.29.1k.
OS Human adenovirus 8 (HADV-8).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=31545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=H16;
RX PubMed=12560390; DOI=10.1136/jcp.56.2.120;
RA Adhikary A.K., Numaga J., Kaburaki T., Kawashima H., Araie M.,
RA Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukoyama A., Matsuno S.,
RA Inada T., Okabe N.;
RT "Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
RT City over a 15-year Period.";
RL J. Clin. Pathol. 56:120-125(2003).
DR EMBL: AB102672; BAC78834.1; -; Genomic DNA.
SQ SEQUENCE 259 AA; 29138 MW; D3742E9ADBAC5CF4 CRC64;

Query Match      16.4%; Score 90.5; DB 2; Length 259;
Best Local Similarity 22.5%; Pred. No. 0.14;
Matches 18; Conservative 23; Mismatches 26; Indels 13; Gaps 2;

Qy 9 TTDYRNTTATGLTSALNLPQVHAFVND-----WASLDMMWFSTALMFVCLIIIM 56

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 19:43:21 ; Search time 16 Seconds  
(without alignments)  
607.368 Million cell updates/sec

Title: US-10-822-873-11  
Perfect score: 551  
Sequence: 1 MTGSTAPTDRYNTATG.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	346	62.8	93	1 ERAD53	early E3A 10.5K pr
2	77	14.0	235	2 I50610	T-cell surface gly
3	74	13.4	544	2 S52477	disintegrin (EC 3
4	72	13.1	316	2 S50336	NADH2 dehydrogenas
5	70	12.7	324	2 T01316	epoxide hydrolase
6	70	12.7	748	2 S66129	disintegrin (EC 3
7	69.5	12.6	95	2 S72597	hypothetical prote
8	69.5	12.6	518	2 AG0784	rtm protein [impor
9	68	12.3	429	2 AH2409	hypothetical prote
10	67.5	12.3	340	2 T28767	hypothetical prote
11	67.5	12.3	1187	2 T19413	hypothetical prote
12	67	12.2	491	2 S52320	disintegrin (EC 3
13	67	12.2	522	2 A46103	transmembrane gly
14	67	12.2	533	2 T19416	hypothetical prote
15	66.5	12.1	428	2 T48284	hypothetical prote
16	66	12.0	244	2 T22046	hypothetical prote
17	65.5	11.9	306	2 T19412	hypothetical prote
18	65	11.8	279	2 S42125	hypothetical prote
19	65	11.8	466	2 S52258	copper resistance
20	64.5	11.7	242	2 T22922	hypothetical prote
21	64.5	11.7	871	1 I48696	protein-tyrosine k
22	64.5	11.7	881	1 I48697	protein-tyrosine k
23	64	11.6	518	1 G99804	multidrug-efflux t
24	63.5	11.5	83	2 T36483	probable membrane
25	63.5	11.5	150	2 E96521	protein F21D18.14
26	63.5	11.5	254	2 F87652	hypothetical prote
27	63.5	11.5	501	2 T14339	sucrose-proton tra
28	63.5	11.5	638	2 H82690	hypothetical prote
29	63.5	11.5	1667	2 T15863	hypothetical prote

30	63	11.4	138	1 Q0BEB2	UL73 glycoprotein
31	63	11.4	389	2 S67506	large surface anti
32	63	11.4	458	2 S61974	SSu1 protein - yea
33	63	11.4	462	2 C70597	hypothetical prote
34	63	11.4	844	2 T00529	hypothetical prote
35	62.5	11.3	137	2 E88382	protein W06E11.6 l
36	62.5	11.3	332	2 T02789	probable membrane
37	62.5	11.3	558	2 E84324	TRK potassium upa
38	62	11.3	162	2 F82493	hypothetical prote
39	62	11.3	256	2 AH1148	hypothetical prote
40	62	11.3	756	2 S74742	exopolysaccharide
41	61.5	11.2	262	2 S47427	E1 membrane glycop
42	61.5	11.2	283	2 T15964	hypothetical prote
43	61.5	11.2	410	2 C36671	mating-type locus
44	61.5	11.2	410	2 D32696	b3 protein - smut
45	61.5	11.2	603	2 B86215	protein T6D22.10 l

ALIGNMENTS

RESULT 1

ERAD53  
early E3A 10.5K protein - human adenovirus 5  
C;Species: Mastadenovirus h5 (human adenovirus 5)  
A;Note: host Homo sapiens (man)  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C;Accession: A05245  
R;Cladaras, C.; Wold, W.S.M.  
Virology 140, 28-43, 1985  
A;Title: DNA sequence of the early E3 transcription unit of adenovirus 5.  
A;Reference number: A94335; MUID:85092388; PMID:2981456  
A;Accession: A05245  
A;Molecule type: DNA  
A;Residues: 1-93 <CLA>  
A;Cross-references: UNIPROT:P17590; UNIPARC:UPI0000037966; GB:X03002; NID:g58503; PIDN:C  
C;Superfamily: adenovirus early E3A 10.5K protein  
C;Keywords: early protein; transmembrane protein

Query Match 62.8%; Score 346; DB 1; Length 93;  
Best Local Similarity 78.3%; Pred. No. 6.2e-31;  
Matches 65; Conservative 6; Mismatches 8; Indels 4; Gaps 1;

Qy	14	NTT-----ATGLTSALNLPQVHAFVNDWASLDMMWFSLMFVCLIIIMWLICCLKRRARP	69
Db	3	NTTNAATAGLTSTTTPQVSFAFNWNLGMWFSIALMFVCLIIIMWLICCLKRRARP	62
Qy	70	PYRPIIIVLNPHNEKTHRLDGLK	92
Db	63	PYSPPIIIVLHPNNDGIHRLDGLK	85

RESULT 2

I50610  
T-cell surface glycoprotein CD8 alpha chain - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: I50610; S33350  
R;Tregaskes, C.A.; Kong, F.K.; Paramithiotis, E.; Chen, C.L.; Ratcliffe, M.J.; Davison, J.; Immunol. 154, 4485-4494, 1995  
A;Title: Identification and analysis of the expression of CD8 alpha beta and CD8 alpha a lymphocytes.  
A;Reference number: I50609; MUID:95238946; PMID:7722305  
A;Accession: I50610  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-235 <TREG>  
A;Cross-references: UNIPROT:Q90770; UNIPARC:UPI000000FBABF; EMBL:Z22726; NID:g488149; PIDN:C  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: glycoprotein

Query Match 14.0%; Score 77; DB 2; Length 235;  
Best Local Similarity 25.2%; Pred. No. 0.55;





```
Matches 27; Conservative 17; Mismatches 26; Indels 44; Gaps 6;
QY 3 GSTI-----APTTDYRN-----TTATG-----LTSALNLPQVHAFVNDWASLDMW 43
Db 621 GRTITLQPSGPNDFRGYCDVFMRCRLVDAGDLARLKKAIKAFSPELYENIAEW--IVAYW 678
QY 44 FSTALMFVCLITMWL-----IC-----CLKRRRARPPIVRP 74
Db 679 WAVLLMGIALIMLMAGFIKCSVHTPSSNPKLPPPKPLGTLKRRRPPQPIQQP 732
RESULT 7
S72597
hypothetical protein B1937_F2.47 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S72597
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Reference number: S72580
A:Accession: S72597
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-95 <SWI>
A:Cross-references: UNIPROT:Q49760; UNIPARC:UPI0000139B2E; EMBL:U00016; NID:G466961; PID:
Query Match 12.6%; Score 69.5; DB 2; Length 95;
Best Local Similarity 29.2%; Pred. No. 1.5;
Matches 14; Conservative 13; Mismatches 20; Indels 1; Gaps 1;
QY 9 TTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIM 56
Db 13 TVFYDAGTANG-TNGISVPVNGFLNWDLSIELWLSGLAFVLQALVM 59
RESULT 8
AG0784
rtn protein [imported] - Salmonella enterica subsp. enterica serovar Typhi (strain CT18)
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AG0784
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AG0784
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-518 <PAR>
A:Cross-references: UNIPARC:UPI0000059BBE; GB:AL513382; PIDN:CAD02597.1; PID:G16503453;
C:Genetics:
A:Gene: rtn
C:Superfamily: probable membrane protein ylaB
Query Match 12.6%; Score 69.5; DB 2; Length 518;
Best Local Similarity 26.4%; Pred. No. 8.1;
Matches 24; Conservative 13; Mismatches 27; Indels 27; Gaps 6;
QY 5 TTA--PTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCL--IIMWLIC 60
Db 203 TVAELPGTFSRQATNGLPKIQI-----YADSWTYNDLWY---ALMLGICISIVAGFIC 254
QY 61 -CLKRRRARP-----PIYRPII 76
Db 255 YFIYALRTRPGKEILTAIKHEQFYVYQPVW 285
RESULT 9
AH2409
```

```
hypothetical protein all4832 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AH2409
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete genomic sequence of the filamentous nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH2409
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-429 <KUR>
A:Cross-references: UNIPROT:Q8YM05; UNIPARC:UPI00000CEC7A; GB:BA000019; PIDN:BAB76531.1;
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all4832
Query Match 12.3%; Score 68; DB 2; Length 429;
Best Local Similarity 21.2%; Pred. No. 9.8;
Matches 24; Conservative 19; Mismatches 36; Indels 34; Gaps 4;
QY 1 MTGSTIAPT-----TDYRN-----TTATGTSALNLPQVH----- 30
Db 128 LFGALAPDPVLASEVQLTDINDKDLRFGLTSEGLNDALAFPPFVYFGLFAIKDDNNW 187
QY 31 AFVNDWASLDMWFSIALMF-----VCLIIIMWLICLKRRRARPPIYRPIVLN 79
Db 188 TWFQKQVAVDLIWAATNALINGFVVAKAIWIDQVKQRSADALMEDFIALS 240
RESULT 10
T28767
hypothetical protein W03D2.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28767
R:Rohlfing, T.; Wohlmann, P.
submitted to the EMBL Data Library, June 1997
A:Description: The sequence of C. elegans cosmid W03D2.
A:Reference number: Z20519
A:Accession: T28767
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-340 <ROH>
A:Cross-references: UNIPROT:Q45217; UNIPARC:UPI000007BBD5; EMBL:AF000298; PIDN:AAC48262.1
A:Experimental source: strain Bristol N2; clone W03D2
C:Genetics:
A:Gene: CESP:W03D2.10
A:Map position: 4
A:Introns: 63/3; 118/2; 185/3; 210/3; 253/3; 314/1
Query Match 12.3%; Score 67.5; DB 2; Length 340;
Best Local Similarity 25.0%; Pred. No. 8.7;
Matches 21; Conservative 16; Mismatches 30; Indels 17; Gaps 4;
QY 19 GLTSALNLPQ-----VHAFVNDWASLDMWWSF--IALMFVCLIIIMWLICLKRRAR 68
Db 53 GLVEVLTLPERVIVHAGSASVLFVDSFLYEKWIANPLAALYACSPALCITLL-----AS 107
QY 69 PPIYRPIIIVLNPHNKHRLDGLK 92
Db 108 HFVFRYIAVCRPHD--LHHLEGWK 129
RESULT 11
T19413
hypothetical protein C23H4.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19413
R:Wilkinson, J.
```

submitted to the EMBL Data Library, August 1996

A:Accession: T19121  
A:Reference number: Z19121  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-1187 <WIL>  
A:Cross-references: UNIPROT:Q93254; UNIPARC:UPI000017B7AA; EMBL:Z78416; PIDN:CAB01680.1;  
A:Experimental source: clone C23H4  
C:Genetics:  
A:Gene: CESP:C23H4.3  
A:Map position: X  
A:Introns: 48/3; 81/2; 114/3; 182/1; 278/3; 346/3; 401/1; 486/1; 538/3; 635/3; 668/2; 70

Query Match 12.3%; Score 67.5; DB 2; Length 1187;  
Best Local Similarity 22.4%; Pred. No. 31;  
Matches 19; Conservative 15; Mismatches 34; Indels 17; Gaps 3;

QY 4 STIAP--TTDYRNTTATGTSALNLPQV-----HAFVNDWASLDMWFSIALMFVCI 54  
Db 560 SIVEPRTTAHANNATGISTSTNVLTSTAQVISREKFNSTPILQQWFWYLIILVWMI 619

QY 55 IMWLICLKR-----ARPI 71

Db 620 FVLIFISLRPRREESVPPKPPV 644

#### RESULT 12

S52920  
disintegrin (EC 3.4.24.-) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 06-Jun-1995 #sequence\_revision 21-Jul-1995 #text\_change 15-Mar-2004  
A:Accession: S52920; PC4265  
R:Howard, L.; Lu, X.; Mitchell, S.; Griffiths, S.; Glynn, P.  
Submitted to the EMBL Data Library, March 1995  
A:Description: Molecular cloning of MADM: a catalytically active mammalian disintegrin  
A:Reference number: S52920  
A:Accession: S52920  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-491 <HOW>

A:Cross-references: UNIPARC:UPI0000150908; EMBL:Z48579  
R:McKie, N.; Edwards, T.; Dallas, D.J.; Houghton, A.; Stringer, B.; Graham, R.; Russell,  
Biochem. Biophys. Res. Commun. 230, 335-339, 1997  
A:Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM  
A:Reference number: PC4263; MUID:97168971; PMID:9016778  
A:Accession: PC4265  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-247 <MCK>  
A:Cross-references: UNIPARC:UPI000017C0E0  
A:Experimental source: articular chondrocyte  
C:Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m  
F:Keywords: hydrolase; metalloproteinase  
F:126-136/Domain: metal-binding #status predicted <MEB>  
F:199-289/Domain: disintegrin homology <DIS>

Query Match 12.28; Score 67; DB 2; Length 491;  
Best Local Similarity 23.5%; Pred. No. 14;  
Matches 27; Conservative 17; Mismatches 27; Indels 44; Gaps 6;

QY 2 TGSTI-----APTIDYRN-----TTATG-----LTSALNLPQVHAFVNDWASLDMW 42  
Db 363 SGRITILQSPGNCDFGVCDFVRCRLVDADGDLARLKAIFSPELYENIAEW--IVAH 420

QY 43 WFSIALMFVCLIMWL-----IC-----CLKRRRARPPIVRP 74

Db 421 WVAALLMGIALIMLMAGFIKICSVHTSSNPKLPPPKPLGTLKRRRPPQIQP 475

#### RESULT 13

A46103  
transmembrane glycoprotein G - Mokola virus  
C:Species: Mokola virus

C:Date: 07-Apr-1994 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

A:Accession: A46103; D46104  
R:Tordo, N.; Bourhy, H.; Sather, S.; Ollo, R.  
Virology 194, 59-69, 1993  
A:Title: Structure and expression in baculovirus of the Mokola virus glycoprotein: an eff  
A:Reference number: A46103; MUID:93242783; PMID:8480429  
A:Accession: A46103  
A:Status: preliminary  
A:Molecule type: genomic RNA  
A:Residues: 1-522 <TOR>  
A:Cross-references: UNIPROT:Q89507; UNIPARC:UPI00000F7438; GB:S59447; NID:G299713; PIDN:J  
A:Note: sequence extracted from NCBI backbone (NCBIN:130538, NCBIP:130541)  
R:Bourhy, H.; Kissi, B.; Tordo, N.  
Virology 194, 70-81, 1993

A:Title: Molecular diversity of the Lysavirus genus.

A:Reference number: A46104; MUID:93242784; PMID:8386891

A:Contents: lyssavirus serotype 3

A:Accession: D46104

A:Status: preliminary

A:Molecule type: genomic RNA

A:Residues: 1-522 <BOU>

A:Cross-references: UNIPARC:UPI00000F7438; GB:S59448; NID:G299715; PIDN:AAB26296.1; PID:G

A:Note: sequence extracted from NCBI backbone (NCBIN:130542, NCBIP:130548)

C:Superfamily: rabies virus spike glycoprotein

Query Match 12.2%; Score 67; DB 2; Length 522;

Best Local Similarity 33.3%; Pred. No. 15;  
Matches 17; Conservative 9; Mismatches 19; Indels 6; Gaps 2;

QY 24 LNLPOVHAFVNDW-ASLDMWF-----STALMFVCLIMWLICLKRRLAR 68

Db 437 LHMPDVHKSVDVLDGLPHWGMILGATIVAFVVLVCLLRVCKRVRERR 487

#### RESULT 14

T19416  
hypothetical protein E01G6.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
A:Accession: T19416; T20408  
R:Wilkinson, J.  
Submitted to the EMBL Data Library, August 1996  
A:Reference number: Z19121  
A:Accession: T19416  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-533 <WIL>  
A:Cross-references: UNIPROT:O17592; UNIPARC:UPI000007A484; EMBL:Z78416; PIDN:CAB01683.1;  
A:Experimental source: clone C23H4  
R:Lloyd, C.  
submitted to the EMBL Data Library, February 1996

A:Reference number: Z19270

A:Accession: T20408

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-533 <WIL>

A:Cross-references: UNIPARC:UPI000007A484; EMBL:Z69717; PIDN:CAA93533.1; GSPDB:GN00028;

C:Genetics:

A:Gene: CESP:E01G6.3

A:Map position: X

A:Introns: 14/1; 54/1; 58/3; 125/3; 162/1; 194/1; 234/1; 295/1; 319/1; 354/2; 403/1; 455/

Query Match 12.2%; Score 67; DB 2; Length 533;

Best Local Similarity 30.1%; Pred. No. 16;  
Matches 22; Conservative 10; Mismatches 29; Indels 12; Gaps 3;

QY 1 MTGSIATPTDYRNTTATGLT-----SALNLPQVHAFVNDWASLDMW---WWFSIALMFV 51

Db 445 MTAFDREVTRQKTSNGTSLTWSPHPGVPILP---TKTNESSFDISSQWFFAIIVV 501

QY 52 CLIMWLICLKR 64

Db 502 ALILFYLIYVLKR 514

**RESULT 15**

T48284  
hypothetical protein T22P11.220 - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: T48284  
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, C.;  
submitted to the Protein Sequence Database, April 2000  
A;Reference number: 224490  
A;Accession: T48284  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-428 <BEV>  
A;Cross-references: UNIPROT:Q91Z39; UNIPARC:UPI000000C613; EMBL:AL162971  
C;Experimentall source: cultivar Columbia; BAC clone T22P11  
C;Genetics:  
A;Map position: 5  
A;Note: T22P11.220

```

Query Match      12.1%; Score 66.5; DB 2; Length 428;
Best Local Similarity 25.0%; Pred. No. 14;
Matches 15; Conservative 11; Mismatches 21; Indels 13; Gaps 2;

QY 32 FVNDWASLDMMWFSAIMFVCLII---MWLICCLK-----RRRARPPYIRPVIIVL 78
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 300 YTDQWVSWNGIIFFLADITCCCAIVFAMVWVGMCCLURETSKTDGKAVGNLAKLPLVRKEFVL 359

```

Search completed: January 18, 2006, 19:48:21  
Job time : 18 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:01:31 ; Search time 3753 Seconds  
(without alignments)  
3827.241 Million cell updates/sec

Title: US-10-822-873-10  
Perfect score: 307  
Sequence: 1 gatgacggctcaaccatcg.....ttctttacagtattgattaa 307

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_gss1:\*
- 10: gb\_gss2:\*
- 11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	196	63.8	739	6	CD364758	CD364758 UI-H-FT2-BU777756 SJEDNPF08
C 2	40.6	13.2	390	5	BU777756	BU777756 SJEDNPF08
C 3	40	13.0	533	2	BF272879	GA_EB001
C 4	38.8	12.6	648	8	DT112306	JGI_ANN01
C 5	38.4	12.5	573	1	AW187495	BNLGH1587
C 6	38.4	12.5	856	7	CO122313	GR_EB030
C 7	38.4	12.5	865	7	CO116311	GR_EB018
C 8	38.2	12.4	571	10	AG974323	Drosophila
C 9	37.6	12.2	598	8	CV926006	RJ040C12
C 10	36.8	12.0	754	9	BZ997163	PUGFJ11TD
C 11	36.8	12.0	802	10	CG4011905	ZMMBB024
C 12	36.8	12.0	882	9	CC4011331	PUHFL42TD
C 13	36.8	12.0	956	10	CG882662	ZMMBB049
C 14	36.4	11.9	768	10	BX214284	Danio rer
C 15	36.4	11.9	991	10	CZ959245	304628 To
C 16	36.2	11.8	331	8	CV949172	Pvrpbv_13
C 17	36.2	11.8	701	8	CV959926	Pvrpbv_81
C 18	36.2	11.8	1025	10	CL990781	ZMMBHf000
C 19	36	11.7	562	11	TA303004P	AL497488 T. brucei
C 20	36	11.7	565	9	BH767271	BMBAC347H
C 21	35.8	11.7	747	5	EX757054	EX757054
C 22	35.6	11.6	747	8	CV951066	Pvrpbv_47

C 23	35.6	11.6	627	10	CW336158	CW336158 104_835_1
C 24	35.6	11.6	693	10	CW296187	CW296187 104_777_1
C 25	35.6	11.6	699	10	CW427119	fbfb001f1
C 26	35.6	11.6	734	10	BX155641	BX155641 Danio rer
C 27	35.4	11.5	845	8	CV907775	PDPrpcd 27
C 28	35.2	11.5	686	6	CD845789	DH0AB0062
C 29	35	11.4	364	1	AI573060	tt69a09.x
C 30	35	11.4	645	9	BZ899030	CH240_15B
C 31	35	11.4	713	8	CK602294	CT02032A2
C 32	34.8	11.3	137	9	BH261969	CH230-177
C 33	34.8	11.3	626	9	BH275362	CH230-761
C 34	34.8	11.3	730	10	BX140275	BX140275 Danio rer
C 35	34.8	11.3	741	6	CF446046	EST682391
C 36	34.4	11.2	195	10	CL279542	Ggal_93d
C 37	34.4	11.2	704	9	BZ193754	CH230-269
C 38	34.4	11.2	786	9	BH733089	BOMBF75TR
C 39	34.2	11.1	553	10	CE614912	tigr-gss-
C 40	34.2	11.1	706	8	CV906572	PDPrpcd 14
C 41	34.2	11.1	710	5	BX269320	BX269320
C 42	34.2	11.1	758	10	AG536301	Mus muscu
C 43	34.2	11.1	844	7	CK160091	FGAS04163
C 44	34	11.1	184	6	CF685536	CCACU16TR
C 45	34	11.1	246	1	AA051869	Cn0055-5

ALIGNMENTS

RESULT 1 CD364758/c  
LOCUS CD364758 739 bp mRNA linear EST 05-AUG-2004  
DEFINITION UI-H-FT2-bjm-j-05-0-UI.s1 NCI CGAP\_FT2 Homo sapiens CDNA clone  
UI-H-FT2-bjm-j-05-0-UI 3', mRNA sequence.  
ACCESSION CD364758  
VERSION CD364758.1 GI:31148848  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 739)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps@mail.nih.gov  
Tissue Procurement: Dr. Gary W. Hunninghake, U of I  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
http://genome.uiowa.edu/distribution/cgap.html  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
1..739  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FT2-bjm-j-05-0-UI"  
/tissue\_type="Alveolar Macrophage"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NCI CGAP\_FT2"  
/note="Organ: Lung; Vector: p773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;  
NCI CGAP FT2 is a subtracted cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage)

(some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; Control 3 hours; Control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; Adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.

TAG TISSUE=Human Lung Alveolar Macrophage  
TAG\_Lib=UI-H-FT2  
TAG\_SEQ=GGCGATGCCG"

Query Match 13.0%; Score 40; DB 2; Length 533;  
 Best Local Similarity 55.9%; Pred. No. 0.29;  
 Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 97 TGTCATGACTGGCGGAGCTTGACATGTGGTGTTCATAGCGCTATGTTGTTG 156  
 DB 82 TTCTATTAAGAGCTGCGCTTTAACAGGTGAAGCCAGTGAAGAGTGTTCATTTGGG 141

QY 157 CCTATTATATATGCTTATTTGTTGCTTAAGCGCAGACGCGCAGACCCCACTTA 216  
 DB 142 AATTGCTGAATGTTCCATATGCGATCCACAGTCGAGTTCAGCCTGAACCCCACTTA 201

QY 217 TAGSCCTATCATGTG 232  
 DB 202 TATGCACATCCTTCTG 217

RESULT 4  
 DT112306/c 648 bp mRNA linear EST 12-AUG-2005  
 LOCUS JGI\_ANNO1937.rev ANNO Pimephales promelas whole (M) Pimephales  
 DEFINITION promelas cDNA clone ANNO1937 3', mRNA sequence.  
 DT112306  
 DT112306.1 GI:72470750  
 EST.  
 Pimephales promelas  
 Pimephales promelas  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Pimephales.  
 1 (bases 1 to 648)  
 Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C.,  
 Brokstein, P., and Lindquist, E.A.  
 DOE Joint Genome Institute Pimephales promelas EST project  
 Unpublished (2005)  
 Other ESTs: JGI ANNO1937.fwd  
 Contact: Lindquist, E.A., Richardson, P.  
 DOE Joint Genome Institute  
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 Tel: 925 296 5600  
 Fax: 925 296 5710  
 Email: cdna@jgi-psf.org  
 CDNA Library Preparation: DOE Joint Genome Institute:  
 http://www.jgi.doe.gov  
 DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov  
 Naming Conventions: EST name is generated by the concatenation of  
 the JGI Clone Id and the direction of sequencing. The suffix '.rev'  
 indicates a reverse sequencing read of the insert. It does not  
 necessarily reflect the orientation of the insert.  
 Poly-A: Based upon the presence of a run of 14 or more T residues  
 at the beginning of the sequence, this clone was polyadenylated.  
 The resulting Poly-T sequence has been removed.  
 Plate: ANNO 0021 row: a column: 5  
 High quality sequence stop: 553  
 POLYA=Yes.

FEATURES  
 source  
 1..648  
 /organism="Pimephales promelas"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:90988"  
 /clone="ANNO1937"  
 /tissue\_type="Whole"  
 /dev\_stage="Adult"  
 /clone\_lib="ANNO Pimephales promelas Whole (M)"  
 /note="Vector: pDONR222. The library was made from dt  
 primed cDNA and cloned into Invitrogen vector pDONR222.  
 Poly A RNA were primed with a Biotin-attB2-Oligo(dT)  
 primer (5'- GGCGCGCGCACACTTTGTACAGAAAGTTGGGT (T)19 -3')  
 and the first strand synthesized using Superscript II  
 (Invitrogen). The second strand was synthesized and an  
 attB1 adaptor was ligated to the 5' end (5'-  
 TCGTCGGGCACTTTGTACAAAAGTTGGG -3', and 5'-  
 CCAACTTTTTTGTACAAAGTTGTCCC -3'). The cDNA was size

selected using 1% agarose gel electrophoresis. (L  
 ~0.5-1.2K, M ~1.2-2.5K, H ~2.5K) and then inserted into  
 the vector using site specific recombination (flanking  
 attB sites on cDNA). The work was done at DOE Joint Genome  
 Institute."

ORIGIN  
 Query Match 12.6%; Score 38.8; DB 8; Length 648;  
 Best Local Similarity 64.4%; Pred. No. 0.73;  
 Matches 58; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 98 GTCAATGACTGGCGGAGCTTGACATGTGGTGTTCATAGCGCTATGTTGTTG 157  
 DB 158 GTCGATGTCAGGCTTGACTGACATGTAGTTGTTTCCCTTTTCCATTGTGTCG 99

QY 158 CTTATTATTATGTCGCTTATTGTTGCCTA 187  
 DB 98 CTTATTATTATGTCGCTTATTGTTGTTAATA 69

RESULT 5  
 AW187495  
 LOCUS BNLGHI5871 Six-day Cotton fiber Gossypium hirsutum cDNA 5', mRNA  
 DEFINITION  
 AW187495  
 VERSION AW187495.1 GI:6461931  
 KEYWORDS EST.  
 SOURCE Gossypium hirsutum (upland cotton)  
 ORGANISM Gossypium hirsutum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
 1 (bases 1 to 573)  
 Blewitt, M., Matz, E.C. and Burr, B.  
 ESTs from developing cotton fiber (1999b)  
 Unpublished (1999)  
 Contact: Ben Burr  
 Biology Department  
 Brookhaven National Laboratory  
 Upton, NY 11973, USA  
 Tel: 516-344-3396  
 Fax: 516-344-3407  
 Email: burr@bnl.bnl.gov  
 Seq primer: T3 Primer.  
 Location/Qualifiers  
 source  
 1..573  
 /organism="Gossypium hirsutum"  
 /mol\_type="mRNA"  
 /cultivar="Acala Maxxa"  
 /db\_xref="taxon:3635"  
 /tissue\_type="immature fiber"  
 /dev\_stage="Six days post anthesis"  
 /lab\_host="XL1-Blue"  
 /clone\_lib="Six-day Cotton fiber"  
 /note="Vector: pBluescript II KS+"

ORIGIN  
 Query Match 12.5%; Score 38.4; DB 1; Length 573;  
 Best Local Similarity 55.1%; Pred. No. 0.95;  
 Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 97 TGTCATGACTGGCGGAGCTTGACATGTGGTGTTCATAGCGCTATGTTGTTG 156  
 DB 363 TTCTATTAGGAGCTGCGCTTTAACAGGTGAAGCCAGTGAAGTGTTCATTGTGGG 422

QY 157 CTTATTATTATGTCGCTTATTGTTGCTTAAGCGCAGACGCGCAGACCCCACTTA 216  
 DB 423 AATTGCTGAATGTTCCATATGCGATCCACAGTCGAGTTCAGCCTGAACCCCACTTA 482

QY 217 TAGSCCTATCATGTG 232  
 DB 483 TATGCACATCCTTCTG 498

```
RESULT 6
C0122313
LOCUS      C0122313      856 bp      mRNA      linear      EST 16-JUN-2004
DEFINITION GR_EB03001.f GR_Eb Gossypium raimondii cDNA clone GR_EB03001 5',
            mRNA sequence.
ACCESSION  C0122313
VERSION    C0122313.1 GI:48821000
KEYWORDS   EST.
SOURCE     Gossypium raimondii
ORGANISM   Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.

REFERENCE  1 (bases 1 to 856)
AUTHORS   Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
            Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
            Wing,R.A.
TITLE     Global assembly of Cotton ESTs
JOURNAL   Unpublished (2004)
COMMENT   Contact: Rod A. Wing
            Arizona Genomics Institute
            The University of Arizona
            Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: rwing@genome.arizona.edu
            Plate: 03 row: 0 column: 01.

FEATURES             source
     source          1..856
                     /organism="Gossypium raimondii"
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                     /db_xref="taxon:29730"
                     /clone="GR_EB03001"
                     /tissue_type="floral"
                     /dev_stage="3 to +3 DPA"
                     /lab_host="DH10B"
                     /clone_lib="GR_Eb"
                     /note="vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
                     EcoRV; Library made by Invitrogen with RNA supplied by
                     Wendle lab. Directional cloned into NotI-EV. Colonies
                     plated/picked by AGI. More glycerol clones held in -80."

ORIGIN
Query Match      12.5%; Score 38.4; DB 7; Length 856;
Best Local Similarity 55.1%; Pred. No. 1;
Matches 75; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY  97  TGTCAATGACTGGCGAGCTTGGACATGTGGTGTGTTTCCATAGCGCTTATGTTGTTG 156
Db    370 TTCTATTAGAGCTGGCTTTACAGGTGAAGCAGTGAAGTGTGTTGCAATTTGGG 429

QY  157 CCTTATTATTATGTCCTTATTTGTTCCCTAAAGCCGACGCGCCACCCCACTTA 216
Db    430 AATTGCTGGAATGTTCCATATCGATCCAGAGTCGAGTTTCAGCTGGACCCCACTTA 489

QY  217 TAGCCCTATCATTTGTG 232
Db    490 TATGCACATCCTCTGTG 505

RESULT 7
C0116311
LOCUS      C0116311      865 bp      mRNA      linear      EST 16-JUN-2004
DEFINITION GR_EB018106.r GR_Eb Gossypium raimondii cDNA clone GR_EB018106
            3', mRNA sequence.
ACCESSION  C0116311
VERSION    C0116311.1 GI:48814998
KEYWORDS   EST.
SOURCE     Gossypium raimondii
ORGANISM   Gossypium raimondii
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

RESULT 8
AG974323
LOCUS      AG974323      571 bp      DNA      linear      GSS 01-FEB-2005
DEFINITION Drosophila simulans DNA, clone: DSM1-015001.F.fa, genomic survey
            sequence.
ACCESSION  AG974323
VERSION    AG974323.1 GI:58523216
KEYWORDS   GSS.
SOURCE     Drosophila simulans
ORGANISM   Drosophila simulans
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.

REFERENCE  1
AUTHORS   Hattori,M., Toyoda,A., Murakami,K., Kuroki,Y., Fujiyama,A.,
            Toshio,T.K. and Sakaki,Y.
TITLE     BAC end sequences of Library DNB1
JOURNAL   Unpublished
REFERENCE  2 (bases 1 to 571)
AUTHORS   Hattori,M.
TITLE     Direct Submission
JOURNAL   Submitted (19-JAN-2005) Masahira Hattori, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
```







DEFINITION ZM9990492E18f ZM9990492E18f (HindIII) Zea mays genomic clone  
ACCESSION ZM9990492E18f 5', genomic survey sequence.  
VERSION C8882662  
KEYWORDS C8882662.1 GI:38613671  
SOURCE GSS.  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 956)  
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,  
Zohovetz, V., Fuks, G., Yu, Y., Wang, R. and Messing, J.  
Sequencing of the maize genome at FGI (2003c)  
Unpublished (2003)  
Contact: Bharti, A.K.  
Dr. Joachim Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: T7  
Class: BAC ends  
High quality sequence start: 86.  
Location/Qualifiers  
1..956  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
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/clone="ZM9990492E18"  
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/note="Vector: pUC19; Site\_1: HindIII; Site\_2: HindIII"

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Best Local Similarity 50.0%; Pred. No. 3.3;  
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QY 123 TGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATATATATATGCTTATTTGTT 182  
Db 127 TTTTGTGCTTGTCACTAATTTGTTTTCATATTTTTCGTTATGCTGCTGATTTATC 186  
QY 183 GCCTAAGCGCAGCGCGCGAGCCCGCCATCTATAGGCTATCTGCTCAACCCAC 242  
Db 187 CGTCCAAATTTATTTTGTGAGACTTCCGAGCGAGAGCTATTTTTCGCGAGAAA 246  
QY 243 ACAATGAAATAATCATAGATTGGAGCGGTCTGAAACCATGTTCTCTTTTACAGTATG 302  
Db 247 GAAATATAGCAATAACATAGTTTGAAGAGGTAACCTGAATTTTCTATTATTTCTC 306  
QY 303 ATTA 306  
Db 307 ATTA 310

RESULT 14  
BX214284/c  
LOCUS BX214284 768 bp DNA linear GSS 29-JAN-2003  
DEFINITION Danio rerio genomic clone DKEY-258E20, genomic survey sequence.  
ACCESSION BX214284  
VERSION BX214284.1 GI:28046170  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 768)  
Humphrey, S.J., Huckle, E. and Durham, J.L.

TITLE Direct Submission  
JOURNAL Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
COMMENT humquery@sanger.ac.uk Unpublished  
This sequence was generated from the T7 end of BAC 258E20. 258E20  
is part of the Daniokey BAC Library created by R. Plasterk and N.V.  
Keygene. Further details:  
http://www.sanger.ac.uk/Projects/D\_rerio/  
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1..768  
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/db\_xref="taxon:7955"  
/clone="DKEY-258E20"  
/tissue\_type="testis"  
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ORIGIN  
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Db 231 ACCTTAAGATGATAGTATTTAATAGTCTGTAATGCTATTTGCATTTATGATGTTA 172  
QY 173 CTTATTTTGTGCTTAAAGCGCAGCGCGCCAGCCCGCCATCTATAGGCTATCATTTGTG 232  
Db 171 TATAATCGTTATATATATATGCGGATAGATGATCTCAAAATTAAGTAAATATCGCTTAT 112  
QY 233 CTCACCCACACATGAAAAAATTCATAGA 262  
Db 111 CGCAGCAATGTCTATGACAAATATCACACA 82

RESULT 15  
CZ959245/c  
LOCUS CZ959245 991 bp DNA linear GSS 11-AUG-2005  
DEFINITION 304628 Tomato EcorI BAC Library Lycopersicon esculentum genomic  
clone SL EcorI0001113 3, genomic survey sequence.  
ACCESSION CZ959245  
VERSION CZ959245.1 GI:72310041  
KEYWORDS GSS.  
SOURCE Lycopersicon esculentum (Solanum lycopersicum)  
ORGANISM Lycopersicon esculentum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
1 (bases 1 to 991)  
Mueller, L.A., Buel, R.M., Wang, Y., Tanksley, S.D., Giovannoni, J.J.,  
Van Eck, J. and Stack, S.  
BAC end sequencing from three Solanum lycopersicon libraries  
Unpublished (2005)  
Contact: Lukas Mueller  
Tanksley Lab, Dept. of Plant Breeding  
Cornell University  
251 Emerson Hall, Ithaca, NY 14853, USA  
Tel: 607-255-6557  
Fax: 607-255-6683  
Email: sgn-feedback@sgn.cornell.edu  
Plate: 1 row: 1 column: 13  
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Class: BAC ends  
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High quality sequence stop: 694.  
Location/Qualifiers  
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ORIGIN

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Best Local Similarity 55.6%; Pred. No. 4.5;
Matches 70; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Db 406 GTTTTGTAGGTTTGCAGGTTTAATATCATGCATATATTTTGTATCTATCGTTCAAGGGG 347

Qy 202 CAGACCCCATCTATAGGCTATCATTTGTGCTCAACCCACACAATGAAAAAATTCATAG 261
Db 346 TGAACCTCCATCATCAAACTCTTGTATGATCNAATCATCAGGAGCAGAAAAATATAA 287

Qy 262 ATTGGA 267
Db 286 TTGTGA 281
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Search completed: January 20, 2006, 21:07:43  
Job time : 3759 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 18, 2006, 19:42:01 ; Search time 77 Seconds  
(without alignments)  
576.328 Million cell updates/sec

Title: US-10-822-873-11

Perfect score: 551

Sequence: 1 MTGSTTAPTDTYNTATGL.....NEKIHRLDGLKPCSLLLQYD 101

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_21.\*

1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
9: Geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	551	100.0	101	2	AAW61197
2	551	100.0	101	2	AAW78902
3	551	100.0	101	2	AAW75787
4	551	100.0	101	2	AAW98003
5	551	100.0	101	3	AAW84407
6	551	100.0	101	4	AAW61866
7	551	100.0	101	4	AAW50206
8	551	100.0	101	4	AAW47591
9	551	100.0	101	5	ABG69353
10	551	100.0	101	6	ABU10308
11	551	100.0	101	8	ADI36347
12	551	100.0	101	9	ADV20979
13	551	100.0	101	9	ADW47775
14	547	99.3	101	2	AAW59925
15	545	98.9	101	9	ADW28321
16	459	83.3	95	4	AAW61868
17	458	83.1	87	4	AAW61870
18	428.5	77.8	84	4	AAW61872
19	422	76.6	78	4	AAW61869
20	395	71.7	77	4	AAW61871
21	372	67.5	94	4	AAW61865
22	345	62.8	93	4	AAW61867
23	233	42.3	42	4	AAW61876
24	209	37.9	40	4	AAW61873

25	109	19.8	19	4	AAW61874	Aab61874	Ad2 ADP t
26	76	13.8	172	9	ADZ13436	Adz13436	Human can
27	74	13.4	544	7	ADD45030	Add45030	Rat Prote
28	73.5	13.3	521	7	ABO63032	Abo63032	Klebsiell
29	72	13.1	1248	8	ABM83572	Abm83572	Human dia
30	72	13.1	1274	8	ABM83571	Abm83571	Human dia
31	71	12.9	199	8	ADQ66329	Adq66329	Novel hum
32	71	12.9	199	9	ADZ13434	Adz13434	Human can
33	71	12.9	239	6	ABU60695	Abu60695	Human mat
34	71	12.9	277	3	AAW79207	Aay79207	Membrane-
35	71	12.9	277	6	ABU60694	Abu60694	Human mem
36	71	12.9	277	7	ADP50686	Adf50686	Soluble f
37	71	12.9	282	8	ABM82908	Abm82908	Human dia
38	71	12.9	282	8	ABM82910	Abm82910	Human dia
39	71	12.9	282	8	ABM82909	Abm82909	Human dia
40	71	12.9	282	8	ABM82911	Abm82911	Human dia
41	71	12.9	282	8	ABM82912	Abm82912	Human dia
42	71	12.9	283	2	AAW05809	Aaw05809	Human tum
43	71	12.9	283	2	AAW12659	Aaw12659	Human her
44	71	12.9	283	2	AAW60045	Aaw60045	Human TNF
45	71	12.9	283	2	AAW69238	Aaw69238	Herpesvir

#### ALIGNMENTS

RESULT 1

AAW61197

ID AAW61197 standard; protein; 101 AA.

XX

AC AAW61197;

XX

DT 27-AUG-2003 (revised)

DT 07-DEC-1998 (first entry)

XX

DE Adenovirus death protein.

XX

KW Adenovirus death protein; ADP; vector; hepatoma; cancer;

KW alpha-fetoprotein transcription regulatory element; AFP-TRB;

KW hepatocellular carcinoma; hepatoma; gene therapy; human.

XX

OS Mastadenovirus.

XX

PN W09839465-A2.

XX

PD 11-SEP-1998.

XX

PF 03-MAR-1998; 98WO-US004084.

XX

PR 03-MAR-1997; 97US-0039597P.

PR 02-MAR-1998; 98US-00033428.

XX

PA (CALY-) CALYDON INC.

XX

PI Little AS, Lamparski HG, Henderson DR, Schuur ER;

WPI; 1998-495861/42.

XX

DR N-PSDB; AAV47675.

XX

PT New adenovirus vector, for treating cancers - comprising an adenovirus

PT gene under the transcriptional control of an alpha fetoprotein

PT transcription regulatory element.

PS Claim 29; Page 74; 102pp; English.

XX

CC This is the amino acid of the adenovirus death protein (ADP) of of

CC adenovirus type 2. The ADP coding sequence (see AAV47675), with or

CC without the Y leader, can be introduced into an adenoviral genome, e.g.

CC in the E3 or E4 region. Inclusion of such a coding sequence in an

CC adenoviral vector significantly enhances the extent of cytotoxicity, cell

CC killing and virus production. The invention provides replication-

CC competent adenovirus vectors which preferentially replicate in cells that

CC express alpha-fetoprotein (AFP), particularly hepatoma cells. The vectors

CC comprise at least one adenovirus gene, preferably a gene that contributes  
CC to cytotoxicity, under the transcriptional control of an AFP  
CC transcription regulatory element (see AAV47654-55). The vectors are  
CC useful for conferring selective cytotoxicity to AFP-expressing cells,  
CC especially cancer cells. (Updated on 27-AUG-2003 to correct OS field.)  
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Query Match 100.0%; Score 551; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.5e-61;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101  
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 2  
AAW78902  
ID AAW78902 standard; protein; 101 AA.  
XX  
AC AAW78902;  
XX  
DT 21-DEC-1998 (first entry)  
XX  
DE Adenovirus death protein.  
XX  
KW Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE;  
KW human; promoter; enhancer; vector; cancer; gene therapy; PCR; primer;  
KW adenovirus death protein; ADP.  
XX  
OS Mastadenovirus.  
XX  
PN WO9839467-A2.  
XX  
PD 11-SEP-1998.  
XX  
PF 03-MAR-1998; 98WO-US004133.  
XX  
PR 03-MAR-1997; 97US-0039763P.  
PR 02-MAR-1998; 98US-00033555.  
XX  
PA (CALY-) CALYDON INC.  
XX  
PI Lamparski HG, Henserson DR, Schuur ER;  
XX  
DR WPI; 1998-495862/42.  
DR N-PSDB; AAV52966.  
XX  
PT New adenovirus vectors, particularly for cancer therapy - comprising  
PT adenovirus gene under transcriptional control of carcinoembryonic antigen  
PT transcriptional regulatory element.  
XX  
PS Disclosure; Page 68; 95pp; English.  
XX  
CC This is the amino acid sequence of adenovirus death protein (ADP).  
CC Claimed replication-competent adenovirus (Ad) vectors comprise an Ad gene  
CC under transcriptional control of a CEA-TRE. The vectors can be used to  
CC detect and monitor samples for the presence of cells that allow a CEA-TRE  
CC to function, and to selectively kill such cells, especially malignant  
CC cells. Vectors containing an ADP gene (see AAV52966) may be more potent  
CC than vectors lacking the gene, making possible more effective treatment  
CC and/or lower dosage requirement  
XX  
SQ Sequence 101 AA;

Query Match 100.0%; Score 551; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.5e-61;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101  
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 3  
AAW75787  
ID AAW75787 standard; protein; 101 AA.  
XX  
AC AAW75787;  
XX  
DT 21-DEC-1998 (first entry)  
XX  
DE Adenovirus death protein.  
XX  
KW Probasin transcriptional response element; PB-TRE; rat;  
KW androgen receptor; adenovirus; vector; prostate cancer; gene therapy;  
KW adenovirus death protein; ADP.  
XX  
OS Mastadenovirus.  
XX  
PN WO9839466-A2.  
XX  
PD 11-SEP-1998.  
XX  
PF 03-MAR-1998; 98WO-US004132.  
XX  
PR 03-MAR-1997; 97US-0039762P.  
PR 02-MAR-1998; 98US-00033333.  
XX  
PA (CALY-) CALYDON INC.  
XX  
PI Yu D, Henderson DR, Schuur ER, Lamparski HG;  
XX  
DR WPI; 1998-506369/43.  
DR N-PSDB; AAV57354.  
XX  
PT New adenovirus vectors, particularly for cancer therapy - comprising an  
PT adenovirus gene under transcriptional control of a probasin  
PT transcriptional regulatory element.  
XX  
PS Disclosure; Page 96; 117pp; English.  
XX  
CC This is the amino acid sequence of adenovirus death protein (ADP).  
CC Claimed replication-competent adenovirus (Ad) vectors comprise an Ad gene  
CC under transcriptional control of a probasin transcriptional response  
CC element (PB-TRE, see AAV57334). The vector can be used for detecting  
CC cells that allow a PB-TRE to function, especially cells expressing an  
CC androgen receptor, such as prostate cells. They can be used to confer  
CC selective toxicity to such cells. In particular, the vectors can be used  
CC for treating cancers such as prostate cancer. Ad vectors containing the  
CC ADP gene (see AAV57354) may render the vector more potent, making  
CC possible more effective treatment and/or a lower dosage requirement. An  
CC Ad vector has been constructed that contains the ADP gene under control  
CC of PB-TRE. Cytotoxicity was demonstrated toward LNCaP (prostate  
CC carcinoma) cells  
XX  
SQ Sequence 101 AA;

Query Match 100.0%; Score 551; DB 2; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.5e-61;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
Db 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
Qy 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

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Db 61 CLKRRRPPPIRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
|||||
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ID AAW98003 standard; protein; 101 AA.
XX
XX AAW98003;
AC
XX 17-OCT-2003 (revised)
DT 21-JUN-1999 (first entry)
XX
XX Adenovirus death protein.
XX
XX Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;
KW therapy; adenovirus death protein.
XX
XX Human adenovirus type 2.
OS
XX WO9906576-A1.
PN
XX
XX 11-FEB-1999.
PD
XX
XX 04-AUG-1998; 98WO-US016312.
PF
XX
XX 04-AUG-1997; 97US-0054523P.
PR
XX 02-MAR-1998; 98US-0076545P.
PR
XX 03-AUG-1998; 98US-00127834.
PR
XX
XX (CALY-) CALYDON INC.
PA
XX
XX Yu D, Herdenson DR, Schuur ER;
PI WPI; 1999-153804/13.
XX
XX N-PSDB; AAX24756.
DR
XX
XX New nucleic acid containing the human glandular kallikrein enhancer -
PT providing increased expression of heterologous sequences in prostatic
PT cells, and related adenoviral vectors for treating prostatic cancer.
PT
XX
XX Disclosure; Page 165-166; 179pp; English.
PS
XX
XX This protein comprises the adenovirus death protein (ADP) of adenovirus
CC serotype 2. The invention provides novel adenovirus vectors in which at
CC least one adenovirus gene, preferably one that contributes to
CC cytotoxicity, is placed under transcriptional control of a human
CC glandular kallikrein hKLK2 enhancer transcriptional regulatory element
CC (hKLK2-TRE, see AAX24755). Such vectors are useful for treatment of
CC cancers such as prostate cancer. The ADP gene may render the adenoviral
CC vector more potent, making possible more effective treatment and/or lower
CC dosage requirement. (Updated on 17-OCT-2003 to standardise OS field)
CC
XX
XX Sequence 101 AA;
SQ
Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Qy 61 CLKRRRPPPIRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRPPPIRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
RESULT 5
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ID AAW84407 standard; protein; 101 AA.
XX
XX AAW84407;
AC
Query Match 100.0%; Score 551; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Qy 61 CLKRRRPPPIRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRPPPIRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
RESULT 6
AAB61866
ID AAB61866 standard; protein; 101 AA.
XX
XX AAB61866;
AC
XX
XX 08-MAY-2001 (first entry)
DT
XX
XX Ad2 encoded adenovirus death protein (ADP).
DE
XX Adenovirus death protein; ADP; neoplastic; cell death; cancer therapy;
KW anti-cancer; gene therapy; cytostatic; Ad2.
XX
XX Mastadenovirus.
OS
XX
XX Key Location/Qualifiers
FH Domain 1. .40
FT
```

25-JUL-2000 (first entry)

Amino acid sequence of an adenoviral death protein.

adenoviral vector; adenovirus gene; transcriptional control; transcriptional regulatory element; TRE; adenoviral propagation; death protein; tumour.

Mastadenovirus.

WO200015820-A1.

23-MAR-2000.

10-SEP-1999; 99WO-US020718.

10-SEP-1998; 98US-0099791P.

09-SEP-1999; 99US-00392822.

(CALY-) CALYDON INC.

Yu DC, Henderson DR;

WPI; 2000-271456/23.

N-PSDB; AAZ99937.

Adenovirus vectors comprising cell-status specific response elements useful in gene therapy protocols for the treatment of cancers.

Disclosure; Fig 9; 79pp; English.

The present sequence represents an adenoviral death protein, which is used to construct the vectors of the invention. The specification describes adenoviral vectors which comprise an adenovirus gene under transcriptional control of a cell status specific transcriptional regulatory element (TRE). The TRE is preferably one that is essential for adenoviral propagation. The adenovirus vectors may be used for the treatment of a range of tumours such as lung, stomach, breast, colon and rectum, and uterine and cervix cancers

Sequence 101 AA;

Query Match 100.0%; Score 551; DB 3; Length 101; Best Local Similarity 100.0%; Pred. No. 2.5e-61; Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60

Db 1 MTGSTIAPTDDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60

Qy 61 CLKRRRPPPIRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

Db 61 CLKRRRPPPIRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101

RESULT 6

AAB61866

ID AAB61866 standard; protein; 101 AA.

XX

AC AAB61866;

XX

08-MAY-2001 (first entry)

DT

XX

XX Ad2 encoded adenovirus death protein (ADP).

DE

XX Adenovirus death protein; ADP; neoplastic; cell death; cancer therapy; anti-cancer; gene therapy; cytostatic; Ad2.

KW

XX Mastadenovirus.

OS

XX

Key Location/Qualifiers

FH Domain 1. .40

FT

FT Peptide /note= "putative luminal domain (AAB61873)"  
FT 1..26  
FT /notes= "fragment specifically claimed for"  
FT Domain 41..59  
FT /notes= "transmembrane domain (AAB61874); fragment  
FT specifically claimed for"  
FT Domain 60..101  
FT /notes= "cytoplasmic-nucleoplasmic domain"  
FT 63..70  
FT /notes= "cytosolic basic proline domain (AAB61875)  
FT fragment specifically claimed for"  
FT XX WO200104282-A2.  
FT XX 18-JAN-2001.  
FT XX 12-JUL-2000; 2000WO-US018971.  
FT XX 12-JUL-1999; 99US-00351778.  
FT XX (UYSL-) UNIV SAINT LOUIS.  
FT XX Wold WSM, Toth K, Doronin K, Tollefson AE;  
FT WPI; 2001-103079/11.  
FT Recombinant vector which is replication-competent in a neoplastic cell  
FT and overexpresses an adenovirus death protein, useful in cancer therapy  
FT when used together with replication-defective adenovirus which expresses  
FT an anti-cancer gene.  
FT XX Claim 5; Page 156; 196pp; English.  
XX The invention relates to a recombinant vector (VI) which is replication-  
CC competent in a neoplastic cell and which overexpresses an adenovirus  
CC death protein (ADP). The vector can be used in a method for promoting  
CC death of a neoplastic cell that comprises contacting the neoplastic cell  
CC with at least one VI; and a composition comprising VI and a second  
CC recombinant virus which is: (a) replication defective and which  
CC expresses an anti-cancer gene product, where VI complements replication  
CC of the second recombinant virus; or (b) replication-competent in a  
CC neoplastic cell. VI, together with one or more replication-defective  
CC adenovirus which expresses an anti-cancer gene product, are useful in  
CC cancer therapy. Overexpression of ADP by VI results in faster lysis of  
CC cells and spread of the virus throughout a cell monolayer than viruses  
CC expressing wild-type levels of ADP. The present sequence represents the  
CC amino acid sequence of an ADP encoded by Ad2  
XX SQ Sequence 101 AA;  
Query Match 100.0%; Score 551; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.5e-61;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60  
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60  
QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101  
DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101  
RESULT 7  
ID AAM50206  
XX AAM50206 standard; protein; 101 AA.  
XX AAM50206;  
AC AAM50206;  
XX 11-SEP-2003 (revised)  
DT 07-JAN-2002 (first entry)  
XX Adenovirus death protein.  
DE

XX Adenovirus death protein; uroplakin II; vector;  
KW transcriptional regulatory element; TRE; urothelial cell; bladder cancer;  
KW human; gene therapy.  
XX Human adenovirus type 2.  
OS WO200172994-A2.  
PN 04-OCT-2001.  
XX 21-MAR-2001; 2001WO-US009224.  
XX 24-MAR-2000; 2000US-0191861P.  
PR (CALY-) CALYDON INC.  
PA Yu D, Zhang H, Henderson DR;  
XX WPI; 2001-639229/73.  
XX N-PSDB; AAI70186.  
DR Human urothelial cell specific uroplakin transcriptional regulatory  
XX sequences, useful for producing adenoviral vectors which can be used to  
PT confer selective cytotoxicity to target cells, especially bladder cancer  
PT cells.  
XX Example 6; Fig 12; 147pp; English.  
PS The present sequence is that of the adenovirus death protein (ADP). The  
XX ADP gene coding region (see AAI70186) was obtained by PCR amplification  
CC and used in the construction of adenoviral vectors in which ADP  
CC expression was under the control of a urothelial cell-specific  
CC transcriptional regulatory element (TRE) derived from the human uroplakin  
CC II gene 5' flanking region (see AAI70144). This is an example of  
CC adenoviral vectors of the invention. Such vectors comprise a gene,  
CC preferably an adenovirus gene, under transcriptional control of a  
CC urothelial cell-specific TRE. They display urothelial cell-specific  
CC cytotoxicity, and are used for the specific, targeted gene therapy of  
CC bladder cancer. (Updated on 11-SEP-2003 to standardise OS field)  
XX SQ Sequence 101 AA;  
Query Match 100.0%; Score 551; DB 4; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.5e-61;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60  
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLC 60  
QY 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101  
DB 61 CLKRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101  
RESULT 8  
ID AAB47591  
XX AAB47591 standard; protein; 101 AA.  
XX AAB47591;  
AC AAB47591;  
XX 11-SEP-2003 (revised)  
DT 07-JAN-2002 (first entry)  
XX ADP amino acid sequence.  
DE Adenovirus; ADP; replication-competent; adenoviral vector; TRE;  
KW transcriptional regulatory element; mutation; deletion; IRES; promoter;  
KW internal ribosome entry site; cytotoxic; cancer; bladder.  
XX unidentified adenovirus.  
OS



FN	W0200173093-A2.
XX	
PD	04-OCT-2001.
XX	
PF	21-MAR-2001; 2001WO-US009036.
XX	
PR	24-MAR-2000; 2000US-0192156P.
XX	
PA	(CALY-) CALYDON INC.
XX	
PI	Yu D, Li Y, Henderson DR;
XX	
DR	WPI; 2001-639234/73.
XX	
DR	N-PSDB; AAH43535.
XX	
PT	Replication-competent adenoviral vector, useful e.g. for killing cancer
PT	cells, contains two genes linked by internal ribosome entry site and
PT	controlled by target-specific regulator.
XX	
PS	Disclosure; Fig 9; 148pp; English.
XX	
CC	This sequence represents adenoviral ADP. The ADP coding sequence may be
CC	used in the replication-competent adenoviral vector (A) of the invention
CC	which contains two genes (G1, G2) that are co-transcribed as a single
CC	mRNA and under control of a heterologous, target cell- specific
CC	transcriptional regulatory element ("IRE"). G2 has a mutation in, or
CC	deletion of, its endogenous promoter and is controlled from an internal
CC	ribosome entry site (IRES). The ADP coding sequence may be used as G1 or
CC	G2. (A) has greater specificity for a target cell than a similar vector
CC	in which IRE is operably linked to a gene and which lacks an IRES. (A)
CC	are used to modify the genotype of target cells, optionally in vitro with
CC	subsequent return of altered cells to the host and where G2 is a
CC	cytotoxic gene, to confer selective cytotoxicity to target cells,
CC	especially for killing cancer cells. ADP displays a cytotoxic,
CC	particularly cell lysis, function. Also (A) are used for diagnosis and
CC	monitoring, e.g. detection of bladder cancer cells. The target cell-
CC	specific TRE ensures that (A) has better targeting specificity, with
CC	minimal replication in non-target cells, so a runaway infection is
CC	prevented but production of adenoviral proteins in target cells activates
CC	and/or stimulates the immune response against target cells producing such
CC	proteins. The use of an IRES (rather than two identical control elements)
CC	eliminates the risk of homologous recombination and may provide enough
CC	extra space for an additional (therapeutic) gene. (Updated on 11-SEP-2003
CC	to standardise OS field)
XX	
SQ	Sequence 101 AA;
	Query Match 100.0%; Score 551; DB 4; Length 101;
	Best Local Similarity 100.0%; Pred. No. 2.5e-61;
	Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 MTGSGTIAPTTDYRNTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
Db	1 MTGSGTIAPTTDYRNTATGLTSALNLPQVHAFVNDWASLDMMWFSIALMFVCLIIIMWLIC 60
QY	61 CLKRRRARPPYIRPIIVLNPNEKHRLDGLKPCSLLLQYD 101
Db	61 CLKRRRARPPYIRPIIVLNPNEKHRLDGLKPCSLLLQYD 101
RESULT 9	
ABG69353	
ID	ABG69353 standard; protein; 101 AA.
XX	
AC	ABG69353;
XX	
DT	21-OCT-2002 (first entry)
XX	
DE	Adenovirus death protein (ADP).
XX	
KW	Adenovirus; transcriptional regulatory element; TRE; prostate; liver;
XX	breast cancer; colon cancer; antitumour; adenovirus death protein.
XX	

OS	Unidentified.
XX	
PN	US2002068049-A1.
XX	
PD	06-JUN-2002.
XX	
PX	06-DEC-2000; 2000US-00732169.
XX	
PR	10-SEP-1998; 98US-00151376.
XX	
PA	(HEND/) HENDERSON D R.
PA	(SCHU/) SCHUUR E R.
XX	
PI	Henderson DR, Schuur ER;
XX	
DR	WPI; 2002-582468/62..
DR	N-PSDB; ABK99587.
XX	
PT	Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor growth.
PT	
PT	
XX	
PS	Disclosure; Fig 19; 83pp; English.
XX	
CC	The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of a second cell type-specific TRE, where the first and second cell type-specific TREs are substantially identical. When the vector is introduced into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon cancer cell) it allows the cell type-specific TRE to function, resulting in cytotoxicity. The vector is useful for suppressing tumour growth of a target cell. This sequence represents a polypeptide used in the scope of the invention
XX	
SQ	Sequence 101 AA;
	Query Match 100.0%; Score 551; DB 5; Length 101;
	Best Local Similarity 100.0%; Pred. No. 2.5e-61;
	Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MTGSTIAPTDDYRNTTATGLTSALNLPQHAFVNDWASLDMWFSAIMFVCLIIIMWLIC 60       
Db	1 MTGSTIAPTDDYRNTTATGLTSALNLPQHAFVNDWASLDMWFSAIMFVCLIIIMWLIC 60       
QY	61 CLKRRRARPPYRIPIIVLNPHNEKIHRDLGKPCSLLLQYD 101       
Db	61 CLKRRRARPPYRIPIIVLNPHNEKIHRDLGKPCSLLLQYD 101       
RESULT 10	
ABU10308	ID
XX	ABU10308 standard; protein; 101 AA.
AC	ABU10308;
DT	23-OCT-2003 (revised)
DT	07-AUG-2003 (first entry)
XX	
DE	Adenovirus death protein (ADP).
XX	
KW	Adenoviral vector; adenovirus gene; transcriptional control; TRE;
KW	cell type-specific; transcriptional response element; PSA; hKLK;
KW	prostate-specific antigen; glandular kallikrein; probastatin; PB;
KW	carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUCL1;
KW	cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic;
KW	adenovirus death protein; ADP.
XX	
OS	unidentified adenovirus.
PN	US2003044383-A1.

```

XX 06-MAR-2003.
XX 10-SEP-1998; 98US-00151376.
XX 27-JUN-1995; 95US-00495034.
XX 20-AUG-1996; 96US-00699753.
XX 03-MAR-1997; 97US-0039597P.
XX 03-MAR-1997; 97US-0039599P.
XX 03-MAR-1997; 97US-0039762P.
XX 03-MAR-1997; 97US-0039763P.
XX 02-MAR-1998; 98US-00033333.
XX 02-MAR-1998; 98US-00033428.
XX 02-MAR-1998; 98US-00033555.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX Henderson DR, Schuur ER;
XX WPI; 2003-456547/43.
XX N-PSDB; ACD07312.
XX New adenovirus vector for transfecting target host cells, comprises an
XX adenovirus gene under transcriptional control of a cell type-specific
XX transcriptional response element.
XX Disclosure; Fig 19; 83pp; English.
XX The present invention relates to adenoviral vectors comprising an
XX adenovirus gene under transcriptional control of a cell type-specific
XX transcriptional response element (TRE). Example TREs given in the
XX specification include human prostate-specific antigen (PSA) TRE, human
XX glandular kallikrein (hKLK) TRE, rat probastin (PB) TRE, human
XX carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3
XX (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for
XX introducing new genetic capability, particularly associated with
XX cytotoxicity for treating neoplasia. For example, the vector may be used
XX in a target cell to suppress tumour growth, or to kill the target cell.
XX The vector is particularly useful in gene therapy. The present sequence
XX represents adenovirus death protein (ADP). (Updated on 23-OCT-2003 to
XX standardise OS field)
XX Sequence 101 AA;
XX
Query Match 100.0%; Score 551; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
RESULT 11
ADI36347
ID ADI36347 standard; protein; 101 AA.
XX ADI36347;
XX
XX 22-APR-2004 (first entry)
XX Human ADP protein sequence SeqID 11.
XX human; prostate; transcriptional response element; TRE;
XX polyethylene glycol; PEG; masking agent; tumour cell growth;
XX proliferation; psoriatic lesion; wound healing; hyperplasia; cancer;
XX cytostatic; antipsoriatic; vulnery; ADP.
XX
OS Homo sapiens.
XX US2003152553-A1.
XX 14-AUG-2003.
XX 02-MAY-2002; 2002US-00139089.
XX 27-JUN-1995; 95US-00495034.
XX 26-JUN-1996; 96US-00669753.
XX 03-MAR-1997; 97US-0039597P.
XX 03-MAR-1997; 97US-0039762P.
XX 03-MAR-1997; 97US-0039763P.
XX 02-MAR-1998; 98US-00033333.
XX 02-MAR-1998; 98US-00033428.
XX 02-MAR-1998; 98US-00033555.
XX 10-SEP-1998; 98US-00151376.
XX 02-JUN-2000; 2000US-00509591.
XX (LITT/) LITTLE A S.
XX (LAMP/) LAMPARSKI H G.
XX (HEND/) HENDERSON D R.
XX (SCHU/) SCHUUR E R.
XX Little AS, Lamparski HG, Henderson DR, Schuur ER;
XX WPI; 2004-119002/12.
XX N-PSDB; ADI36417.
XX Composition comprising replication competent adenovirus having adenovirus
XX gene essential for replication under transcriptional control of cell type
XX specific transcriptional response element and masking agent.
XX Disclosure; SEQ ID NO 11; 115pp; English.
XX This invention relates to a novel composition that contains a replication
XX competent adenovirus capable of transfecting target host cells.
XX Specifically, it comprises an adenoviral gene essential for replication
XX (E1A, E1B or E4), which is under the transcriptional control of a
XX prostate specific transcriptional response element (TRE) and polyethylene
XX glycol (PEG) as the masking agent. The present invention describes this
XX composition as useful for suppressing tumour cell growth and for lowering
XX the levels of tumour cell markers. It can also be used for introducing
XX transient expression that may be involved in treating undesired
XX proliferations other than tumours, such as psoriatic lesions and wound
XX healing. In addition, it is useful for detecting cells where a cell type-
XX specific TRE is functional in a biological sample and for treating
XX prostate-associated diseases such as hyperplasia and cancer. As such,
XX these compositions exhibit cytostatic, antipsoriatic and vulnery
XX activities. This polypeptide sequence is the human ADP protein of the
XX invention.
XX Sequence 101 AA;
XX
Query Match 100.0%; Score 551; DB 8; Length 101;
Best Local Similarity 100.0%; Pred. No. 2.5e-61;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
DB 61 CLKRRRARPPIYRPIIIVLNPNEKIHRLDGLKPCSLLLQYD 101
RESULT 12
ADV20979
ID ADV20979 standard; protein; 101 AA.
XX ADV20979;
XX

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DT 24-FEB-2005 (first entry)  
DE Adenovirus death protein (ADP).  
XX  
XX  
XX Vector; gene transfer; cloning vehicle; genetic engineering;  
KW prostate cancer; gene therapy; vaccine; cytostatic;  
KW prostate-specific antigen; TRE; transcriptional regulatory element; PSE;  
KW prostate specific enhancer; PSA; prostate specific antigen; cancer;  
KW adenovirus death protein; ADP.  
XX  
OS unidentified adenovirus.  
XX  
XX US2004241857-A1.  
XX  
XX 02-DEC-2004.  
XX  
XX 13-APR-2004; 2004US-00822873.  
XX  
XX 27-JUN-1995; 95US-00495034.  
PR 26-JUN-1996; 96US-00669753.  
PR 10-SEP-1998; 98US-00151376.  
PR 06-DEC-2000; 2000US-00732169.  
XX  
XX (HEND/) HENDERSON D R.  
PA (SCHU/) SCHUUR E R.  
XX  
XX Henderson DR, Schuur ER;  
PI  
XX WPI; 2005-011642/01.  
DR  
XX New adenovirus vector comprising an adenovirus early gene essential for  
PT propagation under the control of a human prostate specific antigen  
PT promoter and a human prostate specific antigen enhancer, for treating  
PT prostate cancer.  
XX  
XX Disclosure; SEQ ID NO 11; 112pp; English.  
XX  
CC The present invention relates to an adenovirus vector comprising an  
CC adenovirus early gene essential for propagation under the control of a  
CC human prostate specific antigen promoter and a human prostate specific  
CC antigen (PSA) enhancer. The invention is useful for treating a patient  
CC suffering from prostate cancer and for making mammalian hosts that are  
CC transiently transgenic and for detecting the presence of cells that  
CC permit the function of a cell type-specific transcriptional regulatory  
CC element (TRE) in a sample. The invention is also used in the gene therapy  
CC and also as vaccine. The present sequence is the adenovirus death protein  
CC (ADP).  
XX  
SQ Sequence 101 AA;  
Query Match 100.0%; Score 551; DB 9; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.5e-61;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
QY 61 CLKRRRARPPIYRPIIVLNPHEKIHRLDGLKPCSLLLQYD 101  
DB 61 CLKRRRARPPIYRPIIVLNPHEKIHRLDGLKPCSLLLQYD 101  
RESULT 13  
ADW47775  
ID ADW47775 standard; protein; 101 AA.  
XX  
AC ADW47775;  
XX  
DT 07-APR-2005 (first entry)  
XX Adenovirus death protein.  
XX  
XX

KW Gene therapy; vector; prostate tumor; cytostatic; vasotropic; vulneryary;  
KW antipsoriatic; antimicrobial; immunomodulator.  
OS Human adenovirus type 2.  
XX  
XX WO2005007832-A2.  
XX  
XX 27-JAN-2005.  
XX  
XX 24-FEB-2004; 2004WO-US005518.  
XX  
XX 24-FEB-2003; 2003US-0450232P.  
XX  
XX (CELL-) CELL GENESYS INC.  
XX  
XX Harding T, Yu DC;  
XX  
XX WPI; 2005-102098/11.  
DR N-PSDB; ADW47774.  
XX  
XX New replication competent adenovirus vector comprising an inducible  
PT transcriptional transactivator coding sequence and an adenovirus gene,  
PT useful for treating cancer, psoriatic lesions, restenosis or wound  
PT healing.  
XX  
XX Disclosure; SEQ ID NO 11; 66pp; English.  
XX  
CC The present sequence is the protein sequence of adenovirus death protein  
CC (ADP). A claimed replication competent adenovirus vector comprises: an  
CC inducible transcriptional transactivator (TT) coding sequence under the  
CC transcriptional control of a cell type-specific TRE (CT-TRE); and an  
CC adenovirus gene under transcriptional control of a TRE regulated by the  
CC TT, where the TT is functionally responsive to an exogenous inducer  
CC agent. The adenovirus gene is preferably a gene essential for adenoviral  
CC replication. The TT may be inhibited or activated by the inducing agent.  
CC Also claimed is an adenovirus vector comprising: an inducible TT coding  
CC sequence under the transcriptional control of a CT-TRE; and an adenovirus  
CC gene under transcriptional control of a TRE regulated by the TT and a  
CC second gene under transcriptional control of a second TRE, where the TT  
CC is activated by an exogenous inducing agent. The second gene may an  
CC adenoviral gene essential for adenovirus replication, or a transgene such  
CC as a cytotoxic gene. One embodiment of the invention provides adenovirus  
CC vectors in which an adenovirus gene is under transcriptional control of a  
CC first transactivated regulated TRE and a polynucleotide encoding an ADP  
CC under control of a second transactivator regulated TRE, where the  
CC adenovirus gene is essential for replication. Also claimed are host cells  
CC comprising the replication competent adenovirus vector, and methods for  
CC propagating and regulating the vector. A claimed method for selective  
CC cytolysis of a target tumor cell line involves introducing the adenovirus  
CC vector into a cell which allows the CT-TRE to function, and administering  
CC an inducing agent such that the adenovirus vector is propagated and  
CC causes lysis of target prostate cells. The adenovirus vector can also be  
CC used to treat psoriatic lesions, restenosis, wound healing, tissue  
CC repair, enhanced immune response, resistance to infection, production of  
CC factors, enhanced proliferation, investigation of metabolic or other  
CC physiological pathways, or comparison of activity of cells in the  
CC presence and absence of the virus introduced transgene. In vectors of the  
CC invention, expression of a viral gene essential for replication is  
CC regulated both by the CT-TRE and the transactivator regulated TRE, and  
CC indirectly by the concentration of the inducing agent.  
XX  
XX Sequence 101 AA;  
Query Match 100.0%; Score 551; DB 9; Length 101;  
Best Local Similarity 100.0%; Pred. No. 2.5e-61;  
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
DB 1 MTGSTIAPTDDYRNTTATGLTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60  
QY 61 CLKRRRARPPIYRPIIVLNPHEKIHRLDGLKPCSLLLQYD 101  
DB 61 CLKRRRARPPIYRPIIVLNPHEKIHRLDGLKPCSLLLQYD 101

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Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
RESULT 14
AAW59925
ID AAW59925 standard; protein; 101 AA.
XX AC AAW59925;
XX DT 11-JAN-1999 (first entry)
XX DE Adenovirus death protein.
XX KW Adenovirus death protein; ADP; transcription regulatory element; vector;
XX KW breast cancer; prostate cancer; liver cancer; colon cancer; gene therapy.
XX OS Mastadenovirus.
XX PN WO9839464-A2.
XX PD 11-SEP-1998.
XX PF 03-MAR-1998; 98WO-US004080.
XX PR 03-MAR-1997; 97US-0039762P.
XX PR 03-MAR-1997; 97US-0039763P.
XX PR 04-AUG-1997; 97US-0054523P.
XX PR 02-MAR-1998; 98US-00033556.
XX PA (CALY-) CALYDON INC.
XX PI Henderson DR, Yu D, Lamparski HG;
XX DR WPI; 1998-495860/42.
XX DR N-PSDB; AAV53632.
XX PT New adenovirus vectors, used for treating tumours - comprising first and
XX PT second adenovirus genes under control of different heterologous
XX PT transcriptional regulatory elements.
XX PS Disclosure; Page 94; 130pp; English.
XX SS This is the amino acid sequence of adenovirus death protein (ADP). The
XX CC invention provides replication-competent adenovirus vectors specific for
XX CC target cells and methods of using such vectors. The vectors contain
XX CC heterologous transcription regulatory elements (TREs) and may incorporate
XX CC a gene, such as the ADP gene (see AAV53632), which can contribute to
XX CC cytotoxicity in the target cell. Adenoviral replication can be restricted
XX CC to target cells in which the heterologous TREs are functional and thus
XX CC the vectors can provide selective cytotoxicity to the target cells (e.g.
XX CC prostate, liver, breast or colon), particularly neoplastic cells
XX SQ Sequence 101 AA;
Query Match 99.3%; Score 547; DB 2; Length 101;
Best Local Similarity 99.0%; Pred. No. 7.9e-61;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
RESULT 15
ADW28321
ID ADW28321 standard; protein; 101 AA.
XX AC ADW28321;
XX
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```
DT 07-APR-2005 (first entry)
XX Amino acid sequence of adenovirus type 5 adenovirus death protein.
XX Chemothrapy; cytosine deaminase; thymidine kinase; death protein;
XX KW cancer; neoplaam; 5-fluorocytosine; ganciclovir.
XX OS Human adenovirus type 5.
XX PH Key Location/Qualifiers
XX FT Misc-difference 63 /note= "Ala encoded by AAG"
XX FT
XX WO2005007109-A2.
XX PN 27-JAN-2005.
XX PD
XX PF 09-JUL-2004; 2004WO-US022320.
XX PR 09-JUL-2003; 2003US-0486219P.
XX PA (FORD-) FORD HEALTH SYSTEM HENRY.
XX PI Freytag SD, Kim JH, Barton K, Paielli D;
XX DR WPI; 2005-101983/11.
XX DR N-PSDB; ADW28319.
XX PT Novel isolated polynucleotide comprising nucleotide sequence of yeast
XX PT cytosine deaminase/mutant SR 39 herpes simplex virus type 1 thymidine
XX PT kinase fusion gene, useful for treating mammalian patient having
XX PT malignancy or solid tumor.
XX PS Example; Page 54; 62pp; English.
XX SS The specification describes a polynucleotide comprising a nucleotide
XX CC sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus
XX CC type 1 thymidine kinase fusion gene, and further comprising an adenovirus
XX CC type 5 adenovirus death protein gene. The polynucleotide of the invention
XX CC limits the side effects of cancer treatment by using only lower doses of
XX CC radiation. The polypeptide encoded by the above polynucleotide is useful
XX CC for converting 5-fluorocytosine or ganciclovir into active
XX CC chemotherapeutic agents. Pharmaceutical compositions comprising
XX CC recombinant adenoviruses comprising polynucleotides of the invention are
XX CC useful for treating a mammalian patient having a malignancy or solid
XX CC tumor. The present sequence represents an adenovirus type 5 adenovirus
XX CC death protein, which is used to construct polynucleotides of the
XX CC invention.
XX SQ Sequence 101 AA;
Query Match 98.9%; Score 545; DB 9; Length 101;
Best Local Similarity 99.0%; Pred. No. 1.4e-60;
Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
Db 1 MTGSTIAPTTDYRNTTATGTSALNLPQVHAFVNDWASLDMWFSIALMFVCLIIIMWLIC 60
QY 61 CLKRRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
Db 61 CLARRRARPPIYRPIIIVLNPHNEKIHRLDGLKPCSLLLQYD 101
Search completed: January 18, 2006, 19:46:33
Job time : 79 secs
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November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:29:41 ; Search time 391 Seconds  
(without alignments)  
647.192 Million cell updates/sec

Title: US-10-822-873-10

Perfect score: 307

Sequence: 1 gatgacggctcaaacatcg.....ttctttacagtattgataa 307

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6049916 seqs, 412136615 residues

Total number of hits satisfying chosen parameters: 12099832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.New.\*  
1: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
2: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
3: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
4: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
5: /cgn2\_6/prodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
6: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
7: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq1.\*  
8: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
9: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq2.\*  
10: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq3.\*  
11: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	307	100.0	35937	US-11-127-832-3	Sequence 3, Appli
2	196	63.8	35696	US-10-860-436-1	Sequence 1, Appli
3	196	63.8	35893	US-10-860-436-2	Sequence 2, Appli
4	196	63.8	35935	US-11-127-832-4	Sequence 4, Appli
5	196	63.8	35935	US-11-127-832-5	Sequence 5, Appli
6	145	47.2	1172	US-11-066-480-5	Sequence 4, Appli
C 7	35.6	11.6	191350	US-10-857-780-4	Sequence 3556, Ap
C 8	33.2	10.8	2926	US-11-136-527-3556	Sequence 49060, A
9	31.2	10.2	872	US-10-750-185-49060	Sequence 49060, A
10	31.2	10.2	872	US-10-750-623-49060	Sequence 49060, A
11	31	10.1	1542	US-10-750-185-47255	Sequence 47255, A
12	31	10.1	1542	US-10-750-623-47255	Sequence 47255, A
13	30.6	10.0	1009	US-11-136-527-4007	Sequence 4007, Ap
14	30.6	10.0	1009	US-11-136-527-8103	Sequence 8103, Ap
15	30.2	9.8	1691140	US-11-091-018-1	Sequence 1, Appli
C 16	29.4	9.6	928	US-10-750-185-59931	Sequence 59931, A
C 17	29.4	9.6	928	US-10-750-623-59931	Sequence 59931, A
C 18	29.2	9.5	567	US-11-052-554A-575	Sequence 575, App
C 19	29.2	9.5	2563	US-10-750-185-53160	Sequence 53160, A
C 20	29.2	9.5	2563	US-10-750-623-53160	Sequence 53160, A
C 21	29.2	9.5	3486	US-10-750-185-42580	Sequence 42580, A
C 22	29.2	9.5	3486	US-10-750-623-42580	Sequence 42580, A

## ALIGNMENTS

## RESULT 1

US-11-127-832-3  
; Sequence 3, Application US/11127832  
; Publication No. US2006000884A1  
; GENERAL INFORMATION:  
; APPLICANT: Hearing, Patrick  
; APPLICANT: Bahou, Wadie  
; APPLICANT: Sandalon, Ziv  
; APPLICANT: Gnatenko, Dmitri  
; TITLE OF INVENTION: Adenoviral Vectors  
; FILE REFERENCE: STONYB-04970  
; CURRENT APPLICATION NUMBER: US/11/127,832  
; CURRENT FILING DATE: 2005-05-12  
; PRIOR APPLICATION NUMBER: US/09/782,378  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: 60/237,747  
; PRIOR FILING DATE: 2000-10-02  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 3  
; LENGTH: 35937  
; TYPE: DNA  
; ORGANISM: Human adeno-associated virus 2  
US-11-127-832-3

Query Match 100.0%; Score 307; DB 8; Length 35937;  
Best Local Similarity 100.0%; Pred. No. 1.9e-96;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATGACGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  
DB 29467 GATGACGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 29526  
QY 61 AACATCTGCGCTTAAATTTACCCCAAGTTTCATCGCTTTGTCAATGACTGGCGAGCTTGGGA 120  
DB 29527 AACATCTGCGCTTAAATTTACCCCAAGTTTCATCGCTTTGTCAATGACTGGCGAGCTTGGGA 29586  
QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTCCTTATATATGTCGCTTATTTG 180  
DB 29587 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGTTCCTTATATATGTCGCTTATTTG 29646  
QY 181 TTGCGCTTAAAGCCGACAGCGCCAGACCCCGCCATCTATAGCGCTTATCATTTGTGCTCAACCC 240  
DB 29647 TTGCGCTTAAAGCCGACAGCGCCAGACCCCGCCATCTATAGCGCTTATCATTTGTGCTCAACCC 29706

Qy	241	ACACATGAAAAAATTCATAGATTGGAACGGTCTGAAACCATGTTCTCTCTCTTTTACAGTA	300
Db	29707	ACACATGAAAAAATTCATAGATTGGAACGGTCTGAAACCATGTTCTCTCTCTTTTACAGTA	29766
Qy	301	TGATTAA	307
Db	29767	TGATTAA	29773

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RESULT 2
US-10-860-436-1
; Sequence 1, Application US/10860436
; Publication No. US20050271622A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jianfeng
; APPLICANT: Ma, Ding
; APPLICANT: Lu, Yunping
; APPLICANT: Wang, Shixuan
; APPLICANT: Chen, Gang
; APPLICANT: Gao, Ginglei
; TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT
; TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 850141.402
; CURRENT APPLICATION NUMBER: US/10/860,436
; CURRENT FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 15
; *SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 35696
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant adenovirus delta920-946ADV5/ASCH6
US-10-860-436-1

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Query Match	63.8%;	Score 196;	DB 7;	Length 35696;
Best Local Similarity	86.4%;	Pred. No. 1.2e-57;		
Matches 228;	Conservative 0;	Mismatches 35;	Indels 1;	Gaps 1;
Qy	45	CCACTGCTACCGGACGAACATCTGCGCCTAAATTTACCCCAAGTTTCATGCGCTTTGTGTCATG	104	
Db	29274	CGCGCGCTACCGGACTTACATCTACCACAAATACACCCCAAGTTTCTGCGCTTTGTGTCATTA	29333	
Qy	105	ACTGGGCGAGCTTGGACATGCTGGTGCTTTTCCATAGGCGCTATGTTTGTGTTGGCTTATTA	164	
Db	29334	ACTGGGATACTTTGGGCATGCTGGTGCTTCCATAGGCGCTATGTTTGTATGCGCTTATTA	29393	
Qy	165	TTATGTGGCTTATTTTGTGTGCTTAAAGCGCAGACGCGCCAGACCCCGCCATCTTAGGCGCTTA	224	
Db	29394	TTATGTGGCTCATCTGTGCTGCTTAAAGCGCAAAACGCGCCCGACCCACATCTATAGTCCCA	29453	
Qy	225	TCATTGTGCTCAACCCACACAAGTAAATAATTCATAGATTGGACGCTGTGAAC-C-CATGT	283	
Db	29454	TCATTGTGCTACACCCCAACAACATGATGGAATCCATAGATTGGACGGACTGAAACACATGT	29513	
Qy	284	TCTCTTCTTTTACAGTAGTATTAA	307	
Db	29514	TCTTTTCTCTTACAGTATGATTAA	29537	

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RESULT 3
US-10-860-436-2
; Sequence 2, Application US/10860436
; Publication NO. US20050271622A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Jianfeng
; APPLICANT: Ma, Ding
; APPLICANT: Lu, Yumping
; APPLICANT: Wang, Shixuan
; APPLICANT: Chen, Gang
; APPLICANT: Gao, Ginglei
; TITLE OF INVENTION: CONSTRUCT OF TUMOR-SELECTIVE RECOMBINANT

```

```

; TITLE OF INVENTION: ADENOVIRUS, METHODS FOR PREPARING THE SAME
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 850141.402
; CURRENT APPLICATION NUMBER: US/10/860,436
; CURRENT FILING DATE: 2004-06-03
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 35893
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: recombinant adenovirus delta920-946ADV5/ASPLK1
US-10-860-436-2

Query Match      63.8%; Score 196; DB 7; Length 35893;
Best Local Similarity 86.4%; Pred. No. 1.2e-57;
Matches 228; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

Qy 45 CCACGTCTACCGGACTTAACATCTGCGCCCTAAATTTACCCCAAGTTTCATGCCCTTTGTCAATG 104
Db 29471 CGCGCGCTACCGGACTTACATCTACACAAATACACCCCAAGTTTCTGCCCTTTGTCAATA 29530

Qy 105 ACTGGCGGAGCTTGGACATGTGGTGGTGTTCCTCATAGCGCTTATGTTCTTTGCCCTATTATA 164
Db 29531 ACTGGGATAACTTGGGCATGTGGTGTCTCTCCATAGCGCTTATGTTCTATGCGCTTATTA 29590

Qy 165 TTATGTGGCTTATTTGTTCCTTAAAGCGGACGCGCCAGACCCCGCATCTATAGGCCTA 224
Db 29591 TTATGTGGCTCATCTGCTGCTTAAAGCGCAACGCGCCCGACCCCATCTATAGTCCCA 29650

Qy 225 TCATCTGCTCAACCCACACAAATGAAAATTCATAGATTGGACGGTCTGAAAC-CATGT 283
Db 29651 TCATGTGCTACACCCAAACAATGATGGATCCATAGATTGGACGGACTGAAACACATGT 29710

Qy 284 TCTCTTCTTTTACAGTATGATTA 307
Db 29711 TCTTTTCTCTTACAGTATGATTA 29734

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RESULT 4
US-11-127-832-4
; Sequence 4, Application US/11127832
; Publication No. US2006000884A1
; GENERAL INFORMATION:
; APPLICANT: Hearing, Patrick
; APPLICANT: Bahou, Wadie
; APPLICANT: Sandalon, Ziv
; APPLICANT: Gnatenko, Dmitri
; TITLE OF INVENTION: Adenoviral Vectors
; FILE REFERENCE: STONYB-04970
; CURRENT APPLICATION NUMBER: US/11/127,832
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US/09/782,378
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/237,747
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 35935
; TYPE: DNA
; ORGANISM: Human adenovirus type 5
US-11-127-832-4

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	Query Match	63.8%	Score 196	DB 8	Length 35935
	Best Local Similarity	86.4% <td>Pred. No. 1.2e-57</td> <td></td> <td></td>	Pred. No. 1.2e-57		
	Matches 228	Conservative	0	Mismatches 35	Indels 1
Qy	45	CCACTGCTACCGGACTTAA	CATCTGCGCTAAATTT	ATCCCAAGTTCAT	CGCTTTGTCAATG 104
Db	29513	CGCGCGCTACCGGACTT	ATCATCTTACACAAATAT	ACACCCCAAGTTC	TGCTTTGTCAATA 29572



RESULT 6  
US-11-066-480-5  
; Sequence 5, Application US/11066480  
; Publication No. US20050282280A1  
; GENERAL INFORMATION:  
; APPLICANT: ENNIST, DAVID LEONARD

RESULT 7  
 US-10-857-780-4/c  
 ; Sequence 4, Application US/10857780  
 ; Publication No. US20050272043A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ROTH, RICHARD B.  
 ; APPLICANT: BRAUN, ANDREAS  
 ; APPLICANT: KAMMERER, STEFAN M.  
 ; APPLICANT: NELSON, MATTHEW ROBERTS  
 ; APPLICANT: RENELAND, RIKARD HENRY  
 ; APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST  
 ; TITLE OF INVENTION: THEREOF  
 ; FILE REFERENCE: SEQ-4069-CP  
 ; CURRENT APPLICATION NUMBER: US/10/857,780  
 ; CURRENT FILING DATE: 2004-05-28  
 ; PRIOR APPLICATION NUMBER: 10/723,681  
 ; PRIOR FILING DATE: 2003-11-25  
 ; PRIOR APPLICATION NUMBER: 60/490,234  
 ; PRIOR FILING DATE: 2003-07-24  
 ; PRIOR APPLICATION NUMBER: 60/525,239  
 ; PRIOR FILING DATE: 2003-11-25  
 ; NUMBER OF SEQ ID NOS: 4962  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 4  
 ; LENGTH: 191350  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (16914)..(16914)  
 ; OTHER INFORMATION: n is a, c, g, or t  
 ; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: (19266)..(19266)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (26334)..(26334)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (34467)..(34472)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (38627)..(38628)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (40555)..(40555)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (57355)..(57355)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (61207)..(61207)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (64980)..(64980)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (64987)..(64987)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (81452)..(81452)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (95893)..(95893)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (103359)..(103359)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (117565)..(117565)  
; OTHER INFORMATION: n is a, c, g, or t  
; US-10-857-780-4

Query Match 11.6%; Score 35.6; DB 7; Length 191350;  
Best Local Similarity 55.7%; Pred. No. 0.35;  
Matches 68; Conservative 0; Mismatches 54; Indels 0; Gaps 0;  
Qy 108 GGGGACCTGGACATGTGGTGTTCATAGCGCTTATGTGTTCATAGCTTATTTGTTGCTTATTATTA 167  
Db 163145 GGGTCTCTTGGCCAAAGGGGTTTGTTCAGTCAGTTGAGGGGTCCTTTGGATTTCCTTT 163086  
Qy 168 TGTGGCTTATTGTGTCTAAAGCGCAGCGCAGACCCCATCTATAGGCTATCA 227  
Db 163085 TATTCCACATTTCTTCTTTTAGCCAAGATCTGCCACAGTCAGCATCAATGGCCAAATTG 163025  
Qy 228 TT 229  
Db 163025 TT 163024

RESULT 8  
US-11-136-527-3556/c  
; Sequence 3556, Application US/11136527

; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AMI01086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3556  
; LENGTH: 2926  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; US-11-136-527-3556

Query Match 10.8%; Score 33.2; DB 8; Length 2926;  
Best Local Similarity 59.6%; Pred. No. 0.31;  
Matches 56; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
Qy 112 GAGCTTGGACATGTGGTGTTCATAGCGCTTATGTGTTCCTTATTATATGTG 171  
Db 1203 GATCCGCGCCTGTGGTGTTCACCTCAGCCTCTGTCTCTGTAACGTAGGACTTTGGG 1144  
Qy 172 GCTTATTGTTCCTAAAGCGCAGACGCGCCAGA 205  
Db 1143 GCTTCTTCTCCCTCAGATCGAGGCCCTGGA 1110

RESULT 9  
US-10-750-185-49060  
; Sequence 49060, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 49060  
; LENGTH: 872  
; TYPE: DNA  
; ORGANISM: Bovine 19866881284640  
; US-10-750-185-49060

Query Match 10.2%; Score 31.2; DB 7; Length 872;  
Best Local Similarity 55.8%; Pred. No. 0.85;  
Matches 60; Conservative 0; Mismatches 48; Indels 0; Gaps 0;  
Qy 81 CCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGGACATGTGTGGTTCATAG 140  
Db 591 CCAAGAGCCTGCGAGGCACAGTCAGGTTTCAGCCTGTAGGCTGTGTGTTCTCTGG 650  
Qy 141 CGTTATGTTTGTTCCTTATTATATGTTGCTTATTTGTTGCTTAA 188  
Db 651 TGCATATCAAAGGATGCTATTTTTCATCTCTCTACCATGTTGCCAA 698

RESULT 10  
US-10-750-623-49060  
; Sequence 49060, Application US/10750623







Db 241 ACAAAATGAAAAAATTCATAGATTGGACGCTCGAAACCATGTTCTCTCTTTACAGTA 300  
Qy 301 TGATTAA 307  
Db 301 TGATTAA 307  
RESULT 2  
US-09-814-292-3  
; Sequence 3, Application US/09814292  
; Patent No. US20020120117A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Zhang, Hong  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING  
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 348022001500  
; CURRENT APPLICATION NUMBER: US/09/814,292  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/191,861  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence for ADP  
US-09-814-292-3  
Query Match 100.0%; Score 307; DB 3; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.3e-91;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACCACTGCTACCGACT 60  
Db 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACCACTGCTACCGACT 60  
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120  
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120  
Qy 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTATTATGTTGCTTATTG 180  
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTATTATGTTGCTTATTG 180  
Qy 181 TTGCCTAAAGCGCAGACGGCCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240  
Db 181 TTGCCTAAAGCGCAGACGGCCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240  
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGCTCGAAACCATGTTCTCTCTTTACAGTA 300  
Db 241 ACACAATGAAAAAATTCATAGATTGGACGCTCGAAACCATGTTCTCTCTTTACAGTA 300  
Qy 301 TGATTAA 307  
Db 301 TGATTAA 307  
RESULT 3  
US-09-875-228-4  
; Sequence 4, Application US/09875228  
; Patent No. US20020136707A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, D.  
; APPLICANT: Henderson, D.R.  
; APPLICANT: Schuur, E.R.  
; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE

; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF  
; FILE REFERENCE: 348022000900  
; CURRENT APPLICATION NUMBER: US/09/875,228  
; CURRENT FILING DATE: 2001-06-05  
; PRIOR APPLICATION NUMBER: 09/127,834  
; PRIOR FILING DATE: 1998-08-03  
; PRIOR APPLICATION NUMBER: 60/076,545  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/054,523  
; PRIOR FILING DATE: 1997-08-04  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Adenovirus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)..(307)  
US-09-875-228-4  
Query Match 100.0%; Score 307; DB 3; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.3e-91;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACCACTGCTACCGACT 60  
Db 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACCACTGCTACCGACT 60  
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120  
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGAGCTTGA 120  
Qy 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTATTATGTTGCTTATTG 180  
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTATTATGTTGCTTATTG 180  
Qy 181 TTGCCTAAAGCGCAGACGGCCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240  
Db 181 TTGCCTAAAGCGCAGACGGCCAGACCCCATCTATAGGCTTATCATTTGCTCAACCC 240  
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGCTCGAAACCATGTTCTCTCTTTACAGTA 300  
Db 241 ACACAATGAAAAAATTCATAGATTGGACGCTCGAAACCATGTTCTCTCTTTACAGTA 300  
Qy 301 TGATTAA 307  
Db 301 TGATTAA 307  
RESULT 4  
US-09-898-883-22  
; Sequence 22, Application US/09898883  
; Patent No. US20020164799A1  
; GENERAL INFORMATION:  
; APPLICANT: Little, Andrew  
; Lamparski, Henry  
; Schuur, Eric  
; Henderson, Daniel  
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS  
; EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/09/898,883
/ APPLICATION NUMBER: US/09/898,883
/ FILING DATE: 02-Jul-2001
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/033,428
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: POLIZZI, CATHERINE M.
/ REGISTRATION NUMBER: 40,130
/ REFERENCE/DOCKET NUMBER: 34802-30004.00
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 813-5600
/ TELEFAX: (415) 494-0792
/ TELEX: 706141 MRSNFOERS SPO
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 307 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 2..304
/ SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-898-883-22

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGACGCGCCCAACGAGCTATCGCAACACCACTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCCAACGAGCTATCGCAACACCACTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 6
US-09-151-376-61
/ Sequence 61, Application US/09151376
/ Publication No. US20030044383A1
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, D.R.
/ TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
/ FILE REFERENCE: 348022000221
/ CURRENT APPLICATION NUMBER: US/09/151,376
/ CURRENT FILING DATE: 1998-09-10
/ EARLIER APPLICATION NUMBER: 08/669,753
/ EARLIER FILING DATE: 1996-06-26
/ EARLIER APPLICATION NUMBER: 08/495,034
/ EARLIER FILING DATE: 1995-06-27
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 61
/ LENGTH: 307
/ TYPE: DNA
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Unknown
US-09-151-376-61

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGCTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGTTCCTTATTTATGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGACGCGCCCAACGAGCTATCGCAACACCACTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCCAACGAGCTATCGCAACACCACTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 5
US-09-151-376-10
/ Sequence 10, Application US/09151376
/ Publication No. US20030044383A1
/ GENERAL INFORMATION:
/ APPLICANT: Henderson, D.R.
/ TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS
/ FILE REFERENCE: 348022000221
/ CURRENT APPLICATION NUMBER: US/09/151,376
/ CURRENT FILING DATE: 1998-09-10
/ EARLIER APPLICATION NUMBER: 08/669,753
/ EARLIER FILING DATE: 1996-06-26
/ EARLIER APPLICATION NUMBER: 08/495,034
/ EARLIER FILING DATE: 1995-06-27
/ NUMBER OF SEQ ID NOS: 71
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Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120  
Qy 121 CATGTGTGCTTTCCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTATTG 180  
Db 121 CATGTGTGCTTTCCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTATTG 180  
Qy 181 TTGCTAAAGCGGAGAGCGCCGACAGCCCGCCATCTATAGGCTTATCATTTGTCTCAACCC 240  
Db 181 TTGCTAAAGCGGAGAGCGCCGACAGCCCGCCATCTATAGGCTTATCATTTGTCTCAACCC 240  
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
Qy 301 TGATTAA 307  
Db 301 TGATTAA 307

## RESULT 7

US-09-814-357-17  
; Sequence 17, Application US/09814357  
; Publication No. US20030068307A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Chen, Yu  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA  
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,  
; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION  
; FILE REFERENCE: 348022001600  
; CURRENT APPLICATION NUMBER: US/09/814,357  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence for ADP  
US-09-814-357-17

Query Match 100.0%; Score 307; DB 3; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.3e-91;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACCACTGCTACCGGACT 60  
Db 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACCACTGCTACCGGACT 60  
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120  
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120  
Qy 121 CATGTGTGCTTTCCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTATTG 180  
Db 121 CATGTGTGCTTTCCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTATTG 180  
Qy 181 TTGCTAAAGCGGAGAGCGCCGACAGCCCGCCATCTATAGGCTTATCATTTGTCTCAACCC 240  
Db 181 TTGCTAAAGCGGAGAGCGCCGACAGCCCGCCATCTATAGGCTTATCATTTGTCTCAACCC 240  
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
Qy 301 TGATTAA 307  
Db 301 TGATTAA 307

## RESULT 8

US-09-814-351-17  
; Sequence 17, Application US/09814351  
; Publication No. US20030148520A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De-Chao  
; APPLICANT: Li, Yuanhao  
; APPLICANT: Henderson, Daniel R.  
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  
; FILE REFERENCE: 348022001700  
; CURRENT APPLICATION NUMBER: US/09/814,351  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Nucleotide sequence for ADP  
US-09-814-351-17

Query Match 100.0%; Score 307; DB 3; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.3e-91;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACCACTGCTACCGGACT 60  
Db 1 GATGACCGGCTCAACCATCGCGCCACACGGACTATCGCAACCACTGCTACCGGACT 60  
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120  
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120  
Qy 121 CATGTGTGCTTTCCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTATTG 180  
Db 121 CATGTGTGCTTTCCATAGCGCTTATGTTTGTTCCTTATTATTATGTCCTATTG 180  
Qy 181 TTGCTAAAGCGGAGAGCGCCGACAGCCCGCCATCTATAGGCTTATCATTTGTCTCAACCC 240  
Db 181 TTGCTAAAGCGGAGAGCGCCGACAGCCCGCCATCTATAGGCTTATCATTTGTCTCAACCC 240  
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
Qy 301 TGATTAA 307  
Db 301 TGATTAA 307

## RESULT 9

US-10-045-116-19  
; Sequence 19, Application US/10045116  
; Publication No. US20030026792A1  
; GENERAL INFORMATION:  
; APPLICANT: Lamparski, Henry  
; Schuur, Eric  
; Henderson, Daniel  
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS  
; EXPRESSING CARCINOEMBRYONIC ANTIGENS AND METHODS OF USE  
; THEREOF  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: PALO ALTO  
; STATE: CA



```
;
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/045,116
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,555A
; FILING DATE: 02-Mar-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30005.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..304
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-045-116-19

Query Match 100.0%; Score 307; DB 5; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGGAATATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACACGGAATATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGCTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATATGCTTATTG 180
Db 121 CATGTGCTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATATGCTTATTG 180
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 10
US-10-222-479-21
; Sequence 21, Application US/10222479
; Publication No. US20030091538A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS
```

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;
; OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/222,479
; FILING DATE: 16-Aug-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/614,495
; FILING DATE: 11-Jul-2000
; APPLICATION NUMBER: 09/033,333
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20007.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELELEX: 706141
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2..304
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-10-222-479-21

Query Match 100.0%; Score 307; DB 5; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.3e-91;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGGAATATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACACGGAATATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGCTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATATGCTTATTG 180
Db 121 CATGTGCTGTTTTCATAGCGCTTATGTTTGTTCCTTATTATATGCTTATTG 180
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307
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RESULT 11

US-10-139-089-10  
; Sequence 10, Application US/10139089  
; Publication No. US20030152553A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, D.R.  
; APPLICANT: Schuur, E.R.  
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS  
; FILE REFERENCE: 34802200221  
; CURRENT APPLICATION NUMBER: US/10/139,089  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 08/669,753  
; PRIOR FILING DATE: 1996-06-26  
; PRIOR APPLICATION NUMBER: 08/495,034  
; PRIOR FILING DATE: 1995-06-27  
; PRIOR APPLICATION NUMBER: 09/509,591  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/151,376  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/033,428  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/039,597  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: 60/039,555  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: 09/033,333  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: 60/039,763  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: 09/033,333  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/039,762  
; PRIOR FILING DATE: 1997-03-03  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 10  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (2)...(304)  
US-10-139-089-10

Query Match 100.0%; Score 307; DB 6; Length 307;

Best Local Similarity 100.0%; Pred. No. 2.3e-91; Mismatches 0; Indels 0; Gaps 0;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATGACCGGCTCAACCATCGCGCCCAACCGGACTATCGCAACCACTGCTACCGGACT 60  
DB 1 GATGACCGGCTCAACCATCGCGCCCAACCGGACTATCGCAACCACTGCTACCGGACT 60  
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120  
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120  
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATTAATGAGCTTATTG 180  
DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATTAATGAGCTTATTG 180  
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240  
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240  
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
QY 301 TGATTAA 307  
DB 301 TGATTAA 307

RESULT 12

US-10-691-045-17  
; Sequence 17, Application US/10691045  
; Publication No. US20040146489A1

US-10-139-089-61

; Sequence 61, Application US/10139089  
; Publication No. US20030152553A1  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, D.R.  
; APPLICANT: Schuur, E.R.  
; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS  
; FILE REFERENCE: 34802200221  
; CURRENT APPLICATION NUMBER: US/10/139,089  
; CURRENT FILING DATE: 2002-05-02  
; PRIOR APPLICATION NUMBER: 08/669,753  
; PRIOR FILING DATE: 1996-06-26  
; PRIOR APPLICATION NUMBER: 08/495,034  
; PRIOR FILING DATE: 1995-06-27  
; PRIOR APPLICATION NUMBER: 09/509,591  
; PRIOR FILING DATE: 2000-06-02  
; PRIOR APPLICATION NUMBER: 09/151,376  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: 09/033,428  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/039,597  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: 09/033,555  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/039,763  
; PRIOR FILING DATE: 1997-03-03  
; PRIOR APPLICATION NUMBER: 09/033,333  
; PRIOR FILING DATE: 1998-03-02  
; PRIOR APPLICATION NUMBER: 60/039,762  
; PRIOR FILING DATE: 1997-03-03  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 61  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Unknown  
US-10-139-089-61

Query Match 100.0%; Score 307; DB 6; Length 307;

Best Local Similarity 100.0%; Pred. No. 2.3e-91; Mismatches 0; Indels 0; Gaps 0;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATGACCGGCTCAACCATCGCGCCCAACCGGACTATCGCAACCACTGCTACCGGACT 60  
DB 1 GATGACCGGCTCAACCATCGCGCCCAACCGGACTATCGCAACCACTGCTACCGGACT 60  
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120  
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGGGAGCTTGA 120  
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATTAATGAGCTTATTG 180  
DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTTATTTATTAATGAGCTTATTG 180  
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240  
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCAATGCTCAACCC 240  
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
QY 301 TGATTAA 307  
DB 301 TGATTAA 307

RESULT 13

US-10-691-045-17  
; Sequence 17, Application US/10691045  
; Publication No. US20040146489A1

<p> ; GENERAL INFORMATION:  ; APPLICANT: Yu, De-Chao  ; APPLICANT: Li, Yuanhao  ; APPLICANT: Henderson, Daniel R.  ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  ; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  ; FILE REFERENCE: 348022001700  ; CURRENT APPLICATION NUMBER: US/10/691,045  ; CURRENT FILING DATE: 2003-10-21  ; PRIOR FILING DATE: 2001-03-21  ; PRIOR FILING DATE: 2001-03-21  ; PRIOR FILING DATE: 2000-03-24  ; NUMBER OF SEQ ID NOS: 35  ; SOFTWARE: FastSeq for Windows Version 4.0  ; SEQ ID NO 17  ; LENGTH: 307  ; TYPE: DNA  ; ORGANISM: Artificial Sequence  ; FEATURE:  ; OTHER INFORMATION: Nucleotide sequence for ADP  US-10-691-045-17 </p>	<p> Query Match 100.0%; Score 307; DB 7; Length 307;  Best Local Similarity 100.0%; Pred. No. 2.3e-91;  Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  DB 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  QY 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  DB 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  QY 301 TGATTAA 307  DB 301 TGATTAA 307 </p>	<p> ; SEQ ID NO 10  ; LENGTH: 307  ; TYPE: DNA  ; ORGANISM: Homo sapiens  ; FEATURE:  ; NAME/KEY: CDS  ; LOCATION: (2)..(304)  US-10-822-873-10 </p>	<p> Query Match 100.0%; Score 307; DB 8; Length 307;  Best Local Similarity 100.0%; Pred. No. 2.3e-91;  Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  DB 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  QY 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  DB 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  QY 301 TGATTAA 307  DB 301 TGATTAA 307 </p>	<p> ; SEQ ID NO 10  ; LENGTH: 307  ; TYPE: DNA  ; ORGANISM: Homo sapiens  ; FEATURE:  ; NAME/KEY: CDS  ; LOCATION: (2)..(304)  US-10-822-873-10 </p>
<p> ; GENERAL INFORMATION:  ; APPLICANT: Yu, De-Chao  ; APPLICANT: Li, Yuanhao  ; APPLICANT: Henderson, Daniel R.  ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  ; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  ; FILE REFERENCE: 348022001700  ; CURRENT APPLICATION NUMBER: US/10/691,045  ; CURRENT FILING DATE: 2003-10-21  ; PRIOR FILING DATE: 2001-03-21  ; PRIOR FILING DATE: 2001-03-21  ; PRIOR FILING DATE: 2000-03-24  ; NUMBER OF SEQ ID NOS: 35  ; SOFTWARE: FastSeq for Windows Version 4.0  ; SEQ ID NO 17  ; LENGTH: 307  ; TYPE: DNA  ; ORGANISM: Artificial Sequence  ; FEATURE:  ; OTHER INFORMATION: Nucleotide sequence for ADP  US-10-691-045-17 </p>	<p> Query Match 100.0%; Score 307; DB 7; Length 307;  Best Local Similarity 100.0%; Pred. No. 2.3e-91;  Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  DB 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  QY 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  DB 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  QY 301 TGATTAA 307  DB 301 TGATTAA 307 </p>	<p> ; SEQ ID NO 10  ; LENGTH: 307  ; TYPE: DNA  ; ORGANISM: Homo sapiens  ; FEATURE:  ; NAME/KEY: CDS  ; LOCATION: (2)..(304)  US-10-822-873-10 </p>	<p> Query Match 100.0%; Score 307; DB 8; Length 307;  Best Local Similarity 100.0%; Pred. No. 2.3e-91;  Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  DB 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  QY 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  DB 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTCTTTTACAGTA 300  QY 301 TGATTAA 307  DB 301 TGATTAA 307 </p>	<p> ; SEQ ID NO 10  ; LENGTH: 307  ; TYPE: DNA  ; ORGANISM: Homo sapiens  ; FEATURE:  ; NAME/KEY: CDS  ; LOCATION: (2)..(304)  US-10-822-873-10 </p>
<p> ; GENERAL INFORMATION:  ; APPLICANT: Yu, De-Chao  ; APPLICANT: Li, Yuanhao  ; APPLICANT: Henderson, Daniel R.  ; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS  ; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE  ; FILE REFERENCE: 348022001700  ; CURRENT APPLICATION NUMBER: US/10/691,045  ; CURRENT FILING DATE: 2003-10-21  ; PRIOR FILING DATE: 2001-03-21  ; PRIOR FILING DATE: 2001-03-21  ; PRIOR FILING DATE: 2000-03-24  ; NUMBER OF SEQ ID NOS: 35  ; SOFTWARE: FastSeq for Windows Version 4.0  ; SEQ ID NO 17  ; LENGTH: 307  ; TYPE: DNA  ; ORGANISM: Artificial Sequence  ; FEATURE:  ; OTHER INFORMATION: Nucleotide sequence for ADP  US-10-691-045-17 </p>	<p> Query Match 100.0%; Score 307; DB 7; Length 307;  Best Local Similarity 100.0%; Pred. No. 2.3e-91;  Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  DB 1 GATGACCGGCTCAACCATCGCGCCACACGAGCTATCGCAACCACTGCTACCGGACT 60  QY 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  DB 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCGCTTTGCTCAATGAGCTGGGGGAGCTTGGGA 120  QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCTTATTTATGTTGCTTATTTG 180  QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCTATATAGGCTTATCATTTGCTCAACCC 240  QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAA</p>			

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Db	61		120
Qy	121	CATGTGCTGGTTTCCATAGCGCTTATGTTTGTTCCTTATTATTATGCTTATTTG	180
Db	121		180
Qy	181	TTGCCCTAAAGCGCAGCGCCAGACCCCCCATCTATAGSCCTATCATTTGCTCAACCC	240
Db	181		240
Qy	241	ACACAATGAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTTCTTTTACAGTA	300
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Qy	301	TGATTAA	307
Db	301		307

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Job time : 806 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 19:14:55 ; Search time 144 Seconds  
(without alignments)  
3789.663 Million cell updates/sec

Title: US-10-822-873-10  
Perfect score: 307  
Sequence: 1 gatgccggctcaaccatcg.....ttctttacatgatgattaa 307

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/H\_COMB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	307	100.0	307	3	US-09-033-428-22
3	307	100.0	307	3	US-09-033-556-9
4	307	100.0	307	3	US-09-614-495-21
5	307	100.0	307	3	US-09-898-883-22
6	307	100.0	307	3	US-09-151-376-10
7	307	100.0	307	3	US-09-151-376-61
8	307	100.0	307	3	US-09-814-351-17
9	307	100.0	307	3	US-09-814-292-3
10	307	100.0	307	3	US-09-392-822A-7
11	307	100.0	307	3	US-09-814-357-17
12	307	100.0	307	3	US-09-875-228-4
13	307	100.0	35937	3	US-09-782-378A-3
14	303.8	99.0	34427	3	US-09-111-911-5
15	196	63.8	32166	3	US-09-562-930-11
16	196	63.8	35408	3	US-08-973-334-3
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18	196	63.8	35408	3	US-08-549-489-3
19	196	63.8	35871	3	US-09-956-335-2
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22	196	63.8	35935	3	US-08-379-452-43
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24	196	63.8	35935	3	US-09-244-752-1

25	196	63.8	35935	3	US-09-245-497-1	Sequence 1, Appli
26	196	63.8	35935	3	US-09-409-670-43	Sequence 43, Appl
27	196	63.8	35935	3	US-09-562-919-1	Sequence 1, Appli
28	196	63.8	35935	3	US-09-782-378A-4	Sequence 4, Appli
29	196	63.8	35935	3	US-09-782-378A-5	Sequence 5, Appli
30	196	63.8	35978	3	US-09-956-335-1	Sequence 1, Appli
31	196	63.8	36620	3	US-09-952-060-30	Sequence 30, Appl
32	196	63.8	37474	3	US-09-952-060-25	Sequence 25, Appl
33	196	63.8	38519	3	US-09-952-060-28	Sequence 28, Appl
34	50	16.3	50	3	US-10-131-827-7472	Sequence 7472, Ap
35	35	11.4	289	3	US-09-007-005-17	Sequence 17, Appl
36	35	11.4	289	3	US-09-244-796-17	Sequence 17, Appl
37	33.8	11.0	116955	3	US-09-949-016-17565	Sequence 17565, A
38	32.6	10.6	27884	3	US-09-949-016-17504	Sequence 12504, A
39	31.8	10.4	601	3	US-09-949-016-17369	Sequence 71369, A
40	31.8	10.4	601	3	US-09-949-016-113176	Sequence 113176, A
41	31.8	10.4	1494	2	US-09-540-236-216	Sequence 216, App
42	31.8	10.4	2882	2	US-08-724-394A-12	Sequence 12, Appl
43	31.8	10.4	99629	3	US-09-596-002-37	Sequence 37, Appl
44	31.8	10.4	152132	3	US-09-949-016-13845	Sequence 13845, A
45	31.8	10.4	152145	3	US-09-949-016-12371	Sequence 12371, A

ALIGNMENTS

RESULT 1  
US-09-033-333-21  
; Sequence 21, Application US/09033333  
; Patent No. 6197293  
; GENERAL INFORMATION:  
; APPLICANT: Yu, De Chao  
; APPLICANT: Schuur, Eric  
; APPLICANT: Henderson, Daniel  
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC  
; TITLE OF INVENTION: FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FASTSEQ for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/033,333  
; FILING DATE: 02-MAR-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Catherine, Polizzi M  
; REGISTRATION NUMBER: 40,130  
; REFERENCE/DOCKET NUMBER: 34802-20007.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 21:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 307 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: Coding Sequence

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; LOCATION: 2...304
; OTHER INFORMATION:
US-09-033-333-21

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
Db 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGATGCGCTTATTTG 180
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGATGCGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGAGCGCCGACGCCCCCATCTATAGGCTTATGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGAGCGCCGACGCCCCCATCTATAGGCTTATGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 2
US-09-033-428-22
; Sequence 22, Application US/09033428
; Patent No. 6254862
; GENERAL INFORMATION:
; APPLICANT: Little, Andrew
; APPLICANT: Lamparski, Henry
; APPLICANT: Schuur, Eric
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC FOR CELLS
; TITLE OF INVENTION: EXPRESSING APHA-FETOPROTEIN AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,428
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: POLIZZI, CATHERINE M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-30004.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141 MRSNFOERS SFO
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 2..304
US-09-033-428-22

Query Match      100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GATGACGGCTCAACCATCGCGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGATGCGCTTATTTG 180
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGATGCGCTTATTTG 180
QY 181 TTGCCTAAAGCGCAGAGCGCCGACGCCCCCATCTATAGGCTTATGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGAGCGCCGACGCCCCCATCTATAGGCTTATGCTCAACCC 240
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCACTGTTCTCTTTTACAGTA 300
QY 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 3
US-09-033-556-9
; Sequence 9, Application US/09033556
; Patent No. 6432700
; GENERAL INFORMATION:
; APPLICANT: Henderson, Daniel R.
; APPLICANT: Yu, De Chao
; TITLE OF INVENTION: ADENOVIRUS VECTORS CONTAINING
; TITLE OF INVENTION: HETEROLOGOUS TRANSCRIPTION REGULATORY ELEMENTS AND METHODS
; TITLE OF INVENTION: OF USING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/033,556
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20010.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
```

```

; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 307 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...304
; OTHER INFORMATION:
US-09-033-556-9

Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACGGCTCAACCATCGCGCCCAACGCGACTATCGCAACCACTGCTACCGGACT 60
DB 1 GATGACGGCTCAACCATCGCGCCCAACGCGACTATCGCAACCACTGCTACCGGACT 60
QY 61 AACATCTGCGCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
DB 61 AACATCTGCGCCTAAATTTACCCCAAGTTCATGCTTTGTCAATGACTGGCGGAGCTTGA 120
QY 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCGCTTAATTATATGTGCGCTTAATTG 180
DB 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCGCTTAATTATATGTGCGCTTAATTG 180
QY 181 TTGCCTAAGCGCAGACGCGCCAGACCCCGCATCTATAGGCGCTATCATGTCCTCAACCC 240
DB 181 TTGCCTAAGCGCAGACGCGCCAGACCCCGCATCTATAGGCGCTATCATGTCCTCAACCC 240
QY 241 ACACAATGAAAAAATTCATAGATTGGACGGCTCTGAAACCATGTTCTTCTTTTACAGTA 300
DB 241 ACACAATGAAAAAATTCATAGATTGGACGGCTCTGAAACCATGTTCTTCTTTTACAGTA 300
QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 4
US-09-614-495-21
; Sequence 21, Application US/09614495
; Patent No. 6436394
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; Schuur, Eric
; Henderson, Daniel
; TITLE OF INVENTION: ADENOVIRUS VECTORS SPECIFIC
; FOR CELLS EXPRESSING ANDROGEN RECEPTOR AND METHODS OF USE
; THEREOF
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/614,495
; FILING DATE: 11-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/033,333
; FILING DATE: <Unknown>

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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/898,883  
FILING DATE: 02-Jul-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/033,428  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: POLIZZZI, CATHERINE M.  
REGISTRATION NUMBER: 40,130  
REFERENCE/DOCKET NUMBER: 34802-30004.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 813-5600  
TELEFAX: (415) 494-0792  
TELEX: 706141 MRSNFOERS SFO  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 307 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 2..304  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-898-883-22

Query Match 100.0%; Score 307; DB 3; Length 307;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60  
DB 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60  
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTGCTTATTTATGCGCTTATTG 180  
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTGCTTATTTATGCGCTTATTG 180  
QY 121 CATGTGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGCGCTTATTG 180  
DB 121 CATGTGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGCGCTTATTG 180  
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240  
DB 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240  
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
QY 301 TGATTAA 307  
DB 301 TGATTAA 307

RESULT 6  
US-09-151-376-10  
Sequence 10, Application US/09151376  
Patent No. 6676935  
GENERAL INFORMATION:  
APPLICANT: Henderson, D.R.  
APPLICANT: Schuur, E.R.  
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS  
FILE REFERENCE: 34802200221  
CURRENT APPLICATION NUMBER: US/09/151.376  
CURRENT FILING DATE: 1998-09-10  
EARLIER APPLICATION NUMBER: 08/669,753  
EARLIER FILING DATE: 1996-06-26  
EARLIER APPLICATION NUMBER: 08/495,034  
EARLIER FILING DATE: 1995-06-27  
NUMBER OF SEQ ID NOS: 71

SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 10  
LENGTH: 307  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (2)..(304)  
US-09-151-376-10  
Query Match 100.0%; Score 307; DB 3; Length 307;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60  
DB 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60  
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTGCTTATTTATGCGCTTATTG 120  
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTGCTTATTTATGCGCTTATTG 120  
QY 121 CATGTGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGCGCTTATTG 180  
DB 121 CATGTGTGGTTTCCATAGCGCTTATGTTTGGCTTATTTATGCGCTTATTG 180  
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240  
DB 181 TTGCCTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240  
QY 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
DB 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
QY 301 TGATTAA 307  
DB 301 TGATTAA 307

RESULT 7  
US-09-151-376-61  
Sequence 61, Application US/09151376  
Patent No. 6676935  
GENERAL INFORMATION:  
APPLICANT: Henderson, D.R.  
APPLICANT: Schuur, E.R.  
TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS  
FILE REFERENCE: 34802200221  
CURRENT APPLICATION NUMBER: US/09/151.376  
CURRENT FILING DATE: 1998-09-10  
EARLIER APPLICATION NUMBER: 08/669,753  
EARLIER FILING DATE: 1996-06-26  
EARLIER APPLICATION NUMBER: 08/495,034  
EARLIER FILING DATE: 1995-06-27  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 61  
LENGTH: 307  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Unknown  
US-09-151-376-61  
Query Match 100.0%; Score 307; DB 3; Length 307;  
Best Local Similarity 100.0%; Pred. No. 1.6e-97;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60  
DB 1 GATGACCGGCTCAACCATCGGCCCAACAGGACTATCGCAACACCACTGCTACCGGACT 60  
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTTGTGCTTATTTATGCGCTTATTG 120



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Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Qy 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCTTATTTATGATGCGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCTTATTTATGATGCGCTTATTTG 180
Qy 181 TTGCCTAAAGCGCAGACGGCGCAGACCCCATCTATAGCCCTCATTTGTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGGCGCAGACCCCATCTATAGCCCTCATTTGTGCTCAACCC 240
Qy 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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## RESULT 8

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US-09-814-351-17
; Sequence 17, Application US/09814351
; Patent No. 6692736
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Li, Yuanhao
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: CELL-SPECIFIC ADENOVIRUS VECTORS
; TITLE OF INVENTION: COMPRISING AN INTERNAL RIBOSOME ENTRY SITE
; FILE REFERENCE: 348022001700
; CURRENT APPLICATION NUMBER: US/09/814,351
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP
US-09-814-351-17
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Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCATCGCGCCCAACGGAATATCGCAACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACGGAATATCGCAACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Qy 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCTTATTTATGATGCGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCTTATTTATGATGCGCTTATTTG 180
Qy 181 TTGCCTAAAGCGCAGACGGCGCAGACCCCATCTATAGCCCTCATTTGTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGGCGCAGACCCCATCTATAGCCCTCATTTGTGCTCAACCC 240
Qy 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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## RESULT 9

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US-09-814-292-3
; Sequence 3, Application US/09814292
; Patent No. 6852528
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Zhang, Hong
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: HUMAN UROTHELIAL CELL SPECIFIC UROPLAKIN
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATORY SEQUENCES, VECTORS COMPRISING
; TITLE OF INVENTION: UROPLAKIN-SPECIFIC TRANSCRIPTIONAL REGULATORY SEQUENCES, AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 348022001500
; CURRENT APPLICATION NUMBER: US/09/814,292
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/191,861
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence for ADP
US-09-814-292-3
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Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCATCGCGCCCAACGGAATATCGCAACCACTGCTACCGGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACGGAATATCGCAACCACTGCTACCGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCAATGCTTTGTCAATGACTGGCGGAGCTTGA 120
Qy 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCTTATTTATGATGCGCTTATTTG 180
Db 121 CATGTGGTGGTTTTCATAGCGCTTAATGTTGTTGCTTATTTATGATGCGCTTATTTG 180
Qy 181 TTGCCTAAAGCGCAGACGGCGCAGACCCCATCTATAGCCCTCATTTGTGCTCAACCC 240
Db 181 TTGCCTAAAGCGCAGACGGCGCAGACCCCATCTATAGCCCTCATTTGTGCTCAACCC 240
Qy 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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## RESULT 10

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US-09-392-822A-7
; Sequence 7, Application US/09392822A
; Patent No. 6900049
; GENERAL INFORMATION:
; APPLICANT: Yu, De Chao
; APPLICANT: Henderson, Daniel
; TITLE OF INVENTION: Adenovirus Vectors Containing Cell
; TITLE OF INVENTION: Status-Specific Response Elements and Methods of Use Thereof
; FILE REFERENCE: CELL-014; 122.1
; CURRENT APPLICATION NUMBER: US/09/392,822A
; CURRENT FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 60/099,791
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 09/392,822
; PRIOR FILING DATE: 1999-09-09
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; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 307  
; TYPE: DNA  
; ORGANISM: Adenovirus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (20)...(304)  
US-09-392-822A-7

Query Match 100.0%; Score 307; DB 3; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.6e-97;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GATGACGGCTCAACCAATGTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
Db 1 GATGACGGCTCAACCAATGTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Qy 121 CATGTGGTGGTTCATAGCGCTTATGTTGTTGCTTATTTATTTATTTATTTATTTATTTATTTATTTG 180
Db 121 CATGTGGTGGTTCATAGCGCTTATGTTGTTGCTTATTTATTTATTTATTTATTTATTTATTTATTTG 180
Qy 181 TTGCTTAAAGCGCAGACGGCGCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 240
Db 181 TTGCTTAAAGCGCAGACGGCGCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 240
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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## RESULT 11

US-09-814-357-17

; Sequence 17, Application US/09814357

; Patent No. 6911200

; GENERAL INFORMATION:

; APPLICANT: Yu, De-Chao

; APPLICANT: Chen, Yu

; APPLICANT: Henderson, Daniel R.

; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA

; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,

; TITLE OF INVENTION: CHEMOTHERAPY AND RADIATION

; FILE REFERENCE: 348022001600

; CURRENT APPLICATION NUMBER: US/09/814,357

; CURRENT FILING DATE: 2001-10-15

; PRIOR APPLICATION NUMBER: 60/192,015

; PRIOR FILING DATE: 2000-03-24

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 307

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Nucleotide sequence for ADP

US-09-814-357-17

Query Match 100.0%; Score 307; DB 3; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.6e-97;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GATGACGGCTCAACCAATGTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
Db 1 GATGACGGCTCAACCAATGTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
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```
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Qy 121 CATGTGGTGGTTCATAGCGCTTATGTTGTTGCTTATTTATTTATTTATTTATTTATTTATTTG 180
Db 121 CATGTGGTGGTTCATAGCGCTTATGTTGTTGCTTATTTATTTATTTATTTATTTATTTATTTG 180
Qy 181 TTGCTTAAAGCGCAGACGGCGCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 240
Db 181 TTGCTTAAAGCGCAGACGGCGCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 240
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307
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## RESULT 12

US-09-875-228-4

; Sequence 4, Application US/09875228

; Patent No. 6916918

; GENERAL INFORMATION:

; APPLICANT: Yu, D.

; APPLICANT: Henderson, D.R.

; APPLICANT: Schuur, E.R.

; TITLE OF INVENTION: A HUMAN GLANDULAR KALLIKREIN ENHANCER, VECTORS COMPRISING THE

; TITLE OF INVENTION: ENHANCER AND METHODS OF USE THEREOF

; FILE REFERENCE: 348022000900

; CURRENT APPLICATION NUMBER: US/09/875,228

; CURRENT FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: 09/127,834

; PRIOR FILING DATE: 1998-08-03

; PRIOR APPLICATION NUMBER: 60/076,545

; PRIOR FILING DATE: 1998-03-02

; PRIOR APPLICATION NUMBER: 60/054,523

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4

; LENGTH: 307

; TYPE: DNA

; ORGANISM: Adenovirus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (2)..(307)

US-09-875-228-4

Query Match 100.0%; Score 307; DB 3; Length 307;

Best Local Similarity 100.0%; Pred. No. 1.6e-97;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GATGACGGCTCAACCAATGTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
Db 1 GATGACGGCTCAACCAATGTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Qy 121 CATGTGGTGGTTCATAGCGCTTATGTTGTTGCTTATTTATTTATTTATTTATTTATTTATTTG 180
Db 121 CATGTGGTGGTTCATAGCGCTTATGTTGTTGCTTATTTATTTATTTATTTATTTATTTATTTG 180
Qy 181 TTGCTTAAAGCGCAGACGGCGCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 240
Db 181 TTGCTTAAAGCGCAGACGGCGCCCAAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 240
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGCTCTGAAACCATGTTCTCTCTTTTACAGTA 300
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; LENGTH: 34427
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: Combining E.coli and Adenovirus Sequences
US-09-111-911-5

Query Match      99.0%; Score 303.8; DB 3; Length 34427;
Best Local Similarity 99.3%; Pred. No. 2.5e-95;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACGAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
Db 1996 GTTGACCGGCTCAACCATCGCGCCCAACGAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 1937

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Db 1936 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 1877

QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTCGCTTATTTATGTTGGCTTATTTG 180
Db 1876 CTTGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTCGCTTATTTATGTTGGCTTATTTG 1817

QY 181 TTGCCTAAAGCGCAGAGCGCGCCAGACCCCGCATCTATAGCCCTATCATTTGTGCTCAACCC 240
Db 1816 TTGCCTAAAGCGCAGAGCGCGCCAGACCCCGCATCTATAGCCCTATCATTTGTGCTCAACCC 1757

QY 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 1756 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 1697

QY 301 TGATTAA 307
Db 1696 TGATTAA 1690

RESULT 15
US-09-562-930-11
; Sequence 11, Application US/09562930
; Patent No. 6835812
; GENERAL INFORMATION:
; APPLICANT: Genotherapeutics Inc.
; APPLICANT: Steiner, Mitchell
; APPLICANT: Wang, Chiang
; APPLICANT: Rinaldy, Augustinus
; APPLICANT: Menon, Rema
; TITLE OF INVENTION: Isolated nucleic acids of the p-hyde family, p-hyde proteins, and
; TITLE OF INVENTION: of inducing susceptibility to induction of cell death in cancer
; FILE REFERENCE: P-2762-US2
; CURRENT APPLICATION NUMBER: US/09/562,930
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 09/302,457
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: US 09/499,817
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 32166
; TYPE: DNA
; ORGANISM: Rat
US-09-562-930-11

Query Match      63.8%; Score 196; DB 3; Length 32166;
Best Local Similarity 86.4%; Pred. No. 1.7e-57;
Matches 228; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 45 CCACTGCTACCGGACTTAACATTCGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATG 104
Db 26180 CCGCCGCTACCGGACTTACATTCACCAAAATACCCCAAGTTTCTGCTTTGTCAATA 26239

QY 105 ACTGGGCGAGCTTGGACATGTGGTGGTTTTTCCATAGCGCTTATGTTTGTTCCTTATTA 164
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; LENGTH: 34427
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
; OTHER INFORMATION: Combining E.coli and Adenovirus Sequences
US-09-111-911-5

Query Match      99.0%; Score 303.8; DB 3; Length 34427;
Best Local Similarity 99.3%; Pred. No. 2.5e-95;
Matches 305; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACGAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 60
Db 1996 GTTGACCGGCTCAACCATCGCGCCCAACGAGTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 1937

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 120
Db 1936 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCGCTTTGTCAATGACTGGCGGAGCTTGGGACT 1877

QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTCGCTTATTTATGTTGGCTTATTTG 180
Db 1876 CTTGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTCGCTTATTTATGTTGGCTTATTTG 1817

QY 181 TTGCCTAAAGCGCAGAGCGCGCCAGACCCCGCATCTATAGCCCTATCATTTGTGCTCAACCC 240
Db 1816 TTGCCTAAAGCGCAGAGCGCGCCAGACCCCGCATCTATAGCCCTATCATTTGTGCTCAACCC 1757

QY 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 1756 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 1697

QY 301 TGATTAA 307
Db 1696 TGATTAA 1690

RESULT 15
US-09-562-930-11
; Sequence 11, Application US/09562930
; Patent No. 6835812
; GENERAL INFORMATION:
; APPLICANT: Genotherapeutics Inc.
; APPLICANT: Steiner, Mitchell
; APPLICANT: Wang, Chiang
; APPLICANT: Rinaldy, Augustinus
; APPLICANT: Menon, Rema
; TITLE OF INVENTION: Isolated nucleic acids of the p-hyde family, p-hyde proteins, and
; TITLE OF INVENTION: of inducing susceptibility to induction of cell death in cancer
; FILE REFERENCE: P-2762-US2
; CURRENT APPLICATION NUMBER: US/09/562,930
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 09/302,457
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: US 09/499,817
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 32166
; TYPE: DNA
; ORGANISM: Rat
US-09-562-930-11

Query Match      63.8%; Score 196; DB 3; Length 32166;
Best Local Similarity 86.4%; Pred. No. 1.7e-57;
Matches 228; Conservative 0; Mismatches 35; Indels 1; Gaps 1;

QY 45 CCACTGCTACCGGACTTAACATTCGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATG 104
Db 26180 CCGCCGCTACCGGACTTACATTCACCAAAATACCCCAAGTTTCTGCTTTGTCAATA 26239

QY 105 ACTGGGCGAGCTTGGACATGTGGTGGTTTTTCCATAGCGCTTATGTTTGTTCCTTATTA 164
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Db	26240	ACTGGGATAACTTGGGCATGTGGTGTCTCCATAGCGCTTATGTTGTATGCGCTTATTA	26299
Qy	165	TTATGTGGCTTATTTGTTCCTAAAGCGCAGACGCCAGACCCGCCATCTATAGGCCTA	224
Db	26300	TTATGTGGCTCATCTGCTGCTAAAGCGCAAGCGCCGACCCCATCTATAGTCCCA	26359
Qy	225	TCATTGTGCTCAACCCACACAATGMAAAATTCATAGATTGGACGGTCTGAAAC-CATGT	283
Db	26360	TCATTGTGCTACACCCCAACAAATGATGGAAATCCATAGATTGGACGGACTGAAACACATGT	26419
Qy	284	TCCTCTCTTTTACAGTATGATTAA	307
Db	26420	TCCTCTCTTTTACAGTATGATTAA	26443

Search completed: January 20, 2006, 21:10:15  
Job time : 147 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 20, 2006, 17:03:15 ; Search time 472 Seconds  
(without alignments)  
4334.874 Million cell updates/sec

Title: US-10-822-873-10  
Perfect score: 307  
Sequence: 1 gatgaccggtcaaccatcg.....ttctttacagtatgattaa 307

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_21.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*
- 14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	307	2	AAV47675
2	307	100.0	307	2	AAV52966
3	307	100.0	307	2	AAV57354
4	307	100.0	307	2	AAV24756
5	307	100.0	307	3	AAZ99937
6	307	100.0	307	4	AAI70186
7	307	100.0	307	5	AAH43535
8	307	100.0	307	6	ABK99587
9	307	100.0	307	8	ACD07312
10	307	100.0	307	12	ADI36397
11	307	100.0	307	12	ADI36417
12	307	100.0	307	14	ADV21029
13	307	100.0	307	14	ADV20978
14	307	100.0	307	14	ADW47774
15	307	100.0	917	14	ADW28317
16	307	100.0	34616	6	ABK49009
17	307	100.0	35209	14	ADW28315
18	307	100.0	35937	6	ABS69881
19	307	100.0	35937	9	ACC70007

20	307	100.0	36335	2	AAQ68003	AAQ68003 Ad2/-ORF6
21	305.4	99.5	307	2	AAV53632	AAV53632 Adenoviru
c 22	303.8	99.0	34427	2	AAV07371	AAV07371 Adenoviru
c 23	303.8	99.0	34427	9	ADA09839	ADA09839 Adenoviru
24	303	98.7	303	14	ADW28319	ADW28319 Nucleotid
25	302.2	98.4	35759	10	ADF60698	ADF60698 Ad6 genom
26	302.2	98.4	35759	13	ADS00148	ADS00148 Human ade
27	196	63.8	32165	3	AAA09092	AAA09092 AdMTV-be
28	196	63.8	32165	3	AAA14723	AAA14723 Nucleotid
29	196	63.8	32166	3	AAA09090	AAA09090 ADFSA-bet
30	196	63.8	32166	4	AAC89170	AAC89170 ADRSVpHYD
31	196	63.8	32166	14	ADM11287	ADM11287 Adenovira
32	196	63.8	32167	3	AAA14803	AAA14803 Nucleotid
33	196	63.8	32167	3	AAZ93332	AAZ93332 Partial s
34	196	63.8	32886	3	AAA09086	AAA09086 ADRSV-bet
35	196	63.8	33592	4	AAC85018	AAC85018 Adenoviru
36	196	63.8	33699	4	AAC85020	AAC85020 Adenoviru
37	196	63.8	33988	4	AAC85023	AAC85023 Adenoviru
38	196	63.8	34302	3	AAZ94163	AAZ94163 Adenoviru
39	196	63.8	34341	4	AAC85019	AAC85019 Adenoviru
40	196	63.8	34448	4	AAC85021	AAC85021 Adenoviru
41	196	63.8	34737	4	AAC85024	AAC85024 Adenoviru
42	196	63.8	35408	2	AAV59272	AAV59272 Recombina
43	196	63.8	35620	14	ADY80723	ADY80723 DNA seque
44	196	63.8	35700	14	ADY93032	ADY93032 Human ade
45	196	63.8	35712	14	ADZ45246	ADZ45246 Human ade

ALIGNMENTS

RESULT 1  
AAV47675  
ID AAV47675 standard; DNA; 307 BP.

XX AAV47675;

XX 27-AUG-2003 (revised)  
DT 07-DEC-1998 (first entry)

XX Adenovirus death protein gene.

XX Adenovirus death protein; ADP; vector; hepatoma; cancer;  
KW alpha-fetoprotein transcription regulatory element; AFP-TRE;  
KW hepatocellular carcinoma; hepatoma; gene therapy; human; ds.  
OS Mastadenovirus.

XX Key Location/Qualifiers  
FH CDS 2..307  
FT /\*tag= a

XX WO9839465-A2.

XX 11-SEP-1998.

XX 03-MAR-1998; 98WO-US004084.

XX 03-MAR-1997; 97US-0039597P.

XX 02-MAR-1998; 98US-00033428.

XX (CALY-) CALYDON INC.

XX Little AS, Lamparski HG, Henderson DR, Schuur ER;

XX WPI; 1998-495861/42.

XX E-PSDB; AAW61197.

XX New adenovirus vector, for treating cancers - comprising an adenovirus  
PT gene under the transcriptional control of an alpha fetoprotein  
PT transcription regulatory element.

XX Claim 31; Page 74; 102pp; English.

```

XX This nucleotide sequence codes for adenovirus death protein (ADP, see
CC AAW61197) of adenovirus type 2. The ADP coding sequence (with or without
CC the Y leader) can be introduced into an adenoviral genome, e.g. in the E3
CC or E4 region. Inclusion of such a coding sequence in an adenoviral vector
CC significantly enhances the extent of cytotoxicity, cell killing and virus
CC production. The invention provides replication-competent adenovirus
CC vectors which preferentially replicate in cells that express alpha-
CC fetoprotein (AFP), particularly hepatoma cells. The vectors comprise at
CC least one adenovirus gene, preferably a gene that contributes to
CC cytotoxicity, under the transcriptional control of an AFP transcription
CC regulatory element (see AAV47654-55). The vectors are useful for
CC conferring selective cytotoxicity to AFP-expressing cells, especially
CC cancer cells. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match      100.0%; Score 307; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACCACTGCTACCGGACT 60
   |||||||
DB 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACCACTGCTACCGGACT 60
   |||||||

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGGGA 120
   |||||||
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGGGA 120
   |||||||

QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTGGCTTATTATTATGTTGGCTTATTG 180
   |||||||
DB 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTGGCTTATTATTATGTTGGCTTATTG 180
   |||||||

QY 181 TTGCCTAAAGCGGAGAGCGCGCAGACCCCACTATAGGCTTATCATTTGCTTCAACCC 240
   |||||||
DB 181 TTGCCTAAAGCGGAGAGCGCGCAGACCCCACTATAGGCTTATCATTTGCTTCAACCC 240
   |||||||

QY 241 ACACAATGMAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
   |||||||
DB 241 ACACAATGMAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
   |||||||

QY 301 TGATTAA 307
   |||||||
DB 301 TGATTAA 307

RESULT 2
AAV52966
ID AAV52966 standard; DNA; 307 BP.
XX
AC AAV52966;
XX
XX 21-DEC-1998 (first entry)
XX
XX Adenovirus death protein gene coding region.
XX
XX Carcinoembryonic antigen; transcriptional regulatory element; CEA-TRE;
XX human; promoter; enhancer; vector; cancer; gene therapy; PCR; primer;
XX adenovirus death protein; ADP; ds.
XX
XX Mastadenovirus.
XX
XX Key Location/Qualifiers
XX CDS 2..304
XX /*tag= a
XX
XX WO9839467-A2.
XX
XX 11-SEP-1998.
XX
XX 03-MAR-1998; 98WO-US004133.
XX
XX 03-MAR-1997; 97US-0039763P.
XX
PR 02-MAR-1998; 98US-00033555.
XX
XX (CALY-) CALYDON INC.
XX
XX Lamparski HG, Henerson DR, Schuur ER;
XX
XX WPI; 1998-495862/42.
XX
XX P-PSDB; AAW78902.
XX
XX New adenovirus vectors, particularly for cancer therapy - comprising
XX adenovirus gene under transcriptional control of carcinoembryonic antigen
XX transcriptional regulatory element.
XX
XX Disclosure; Page 67-68; 95pp; English.
XX
XX This is the coding region of the adenovirus death protein (ADP, see
XX AAW78902). It can be obtained by PCR amplification (see also AAV52945-
XX 46). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad
XX gene under transcriptional control of a CEA-TRE. The vectors can be used
XX to detect and monitor samples for the presence of cells that allow a CEA-
XX TRE to function, and to selectively kill such cells, especially malignant
XX cells. Vectors containing an ADP gene may be more potent than vectors
XX lacking the gene, making possible more effective treatment and/or lower
XX dosage requirement
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match      100.0%; Score 307; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACCACTGCTACCGGACT 60
   |||||||
DB 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACCACTGCTACCGGACT 60
   |||||||

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGGGA 120
   |||||||
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGGGA 120
   |||||||

QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTGGCTTATTATTATGTTGGCTTATTG 180
   |||||||
DB 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGTTGGCTTATTATTATGTTGGCTTATTG 180
   |||||||

QY 181 TTGCCTAAAGCGGAGAGCGCGCAGACCCCACTATAGGCTTATCATTTGCTTCAACCC 240
   |||||||
DB 181 TTGCCTAAAGCGGAGAGCGCGCAGACCCCACTATAGGCTTATCATTTGCTTCAACCC 240
   |||||||

QY 241 ACACAATGMAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
   |||||||
DB 241 ACACAATGMAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
   |||||||

QY 301 TGATTAA 307
   |||||||
DB 301 TGATTAA 307

RESULT 3
AAV57354
ID AAV57354 standard; DNA; 307 BP.
XX
AC AAV57354;
XX
XX 21-DEC-1998 (first entry)
XX
XX Adenovirus death protein gene coding region.
XX
XX Probasin transcriptional response element; PB-TRE; rat;
XX androgen receptor; adenovirus; vector; prostate cancer; gene therapy;
XX adenovirus death protein; ADP; ss.
XX
XX Mastadenovirus.
XX
XX Key Location/Qualifiers
XX FH
XX CDS
XX
XX WO9839467-A2.
XX
XX 11-SEP-1998.
XX
XX 03-MAR-1998; 98WO-US004133.
XX
XX 03-MAR-1997; 97US-0039763P.
XX

```

```
FT CDS 2. .304
TT /*tag= a
XX
XX WO9839466-A2.
XX
XX 11-SEP-1998.
XX
XX 03-MAR-1998; 98WO-US004132.
XX
XX 03-MAR-1997; 97US-0039762P.
PR 02-MAR-1998; 98US-00033333.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu D, Henderson DR, Schuur ER, Lamparski HG;
XX
XX WPI; 1998-506369/43.
DR P-PSDB; AAW75787.
XX
XX New adenovirus vectors, particularly for cancer therapy - comprising an
PT adenovirus gene under transcriptional control of a probasin
PT transcriptional regulatory element.
XX
XX Disclosure; Page 96; 117pp; English.
XX
XX This is the coding region of the adenovirus death protein (ADP, see
CC AAW75787). It can be obtained by PCR amplification (see also AAV57350-
CC 51). Claimed replication-competent adenovirus (Ad) vectors comprise an Ad
CC gene under transcriptional control of a probasin transcriptional response
CC element (PB-TRE, see AAV57334). The vector can be used for detecting
CC cells that allow a PB-TRE to function, especially cells expressing an
CC androgen receptor, such as prostate cells. They can be used to confer
CC selective toxicity to such cells. In particular, the vectors can be used
CC for treating cancers such as prostate cancer. Ad vectors containing the
CC ADP gene may render the vector more potent, making possible more
CC effective treatment and/or a lower dosage requirement. An Ad vector has
CC been constructed that contains the ADP gene under control of PB-TRE.
CC Cytotoxicity was demonstrated toward LNCaP (prostate carcinoma) cells
XX
XX Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 307; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGTATCGCAACACCACTGCTACCGGACT 60
DB |||||||
DB 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGATGCTGGCGAGCTTGA 120
DB |||||||
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGATGCTGGCGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCCCTATTATTTATGTCGCTTATTG 180
DB |||||||
DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCCCTATTATTTATGTCGCTTATTG 180
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGTCCTCAACCC 240
DB |||||||
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGTCCTCAACCC 240
QY 241 ACACATGAAATAATTCATAGATTGACGCTCTGTAACACCATGTTCTCTTTTACAGTA 300
DB |||||||
DB 241 ACACATGAAATAATTCATAGATTGACGCTCTGTAACACCATGTTCTCTTTTACAGTA 300
QY 301 TGAATTA 307
DB |||||||
DB 301 TGAATTA 307
XX
XX RESULT 4
XX AAX24756
XX ID AAX24756 standard; DNA; 307 BP.
```

```
XX AAX24756;
XX
XX 17-OCT-2003 (revised)
DT 21-JUN-1999 (first entry)
XX
XX DNA encoding adenovirus death protein.
DE
XX Enhancer; glandular kallikrein-1; hGK-1; hKLK2; human; prostate cancer;
KW therapy; adenovirus death protein; ss.
XX
XX Human adenovirus type 2.
OS
XX
XX Key Location/Qualifiers
FH CDS 2. .309
FT /*tag= a
FT /product= "adenovirus death protein"
XX
XX WO9906576-A1.
PN
XX
XX 11-FEB-1999.
PD
XX
XX 04-AUG-1998; 98WO-US016312.
PF
XX
XX 04-AUG-1997; 97US-0054523P.
PR 02-MAR-1998; 98US-0076545P.
PR 03-AUG-1998; 98US-00127834.
XX
XX (CALY-) CALYDON INC.
PA
XX Yu D, Henderson DR, Schuur ER;
PI
XX WPI; 1999-153804/13.
DR P-PSDB; AAW98003.
XX
XX New nucleic acid containing the human glandular kallikrein enhancer -
PT providing increased expression of heterologous sequences in prostatic
PT cells, and related adenoviral vectors for treating prostatic cancer.
XX
XX Disclosure; Page 165; 179pp; English.
XX
XX This polynucleotide encodes the adenovirus death protein (ADP, see
CC AAW98003) of adenovirus serotype 2. The invention provides novel
CC adenovirus vectors in which at least one adenovirus gene, preferably one
CC that contributes to cytotoxicity, is placed under transcriptional control
CC of a human glandular kallikrein hKLK2 enhancer transcriptional regulatory
CC element (hKLK2-TRE, see AAX24755). Such vectors are useful for treatment
CC of cancers such as prostate cancer. The ADP gene may render the
CC adenoviral vector more potent, making possible more effective treatment
CC and/or lower dosage requirement. (Updated on 17-OCT-2003 to standardise
CC OS field)
XX
XX Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 307; DB 2; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGTATCGCAACACCACTGCTACCGGACT 60
DB |||||||
DB 1 GATGACCGGCTCAACCATCGCGCCCAACACGAGTATCGCAACACCACTGCTACCGGACT 60
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGATGCTGGCGAGCTTGA 120
DB |||||||
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGATGCTGGCGAGCTTGA 120
QY 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCCCTATTATTTATGTCGCTTATTG 180
DB |||||||
DB 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGCCCTATTATTTATGTCGCTTATTG 180
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGTCCTCAACCC 240
DB |||||||
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGCCCTATCATTTGTCCTCAACCC 240
```

```
QY 241 ACACATGAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
Db |||||||
QY 241 ACACATGAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
Db |||||||
QY 301 TGATTAA 307
Db |||||||
QY 301 TGATTAA 307
Db |||||||

RESULT 5
AAZ99937
ID AAZ99937 standard; DNA; 307 BP.
XX
AC AAZ99937;
XX
DT 25-JUL-2000 (first entry)
XX
DE DNA encoding an adenoviral death protein.
XX
KW adenoviral vector; adenovirus gene; transcriptional control;
KW transcriptional regulatory element; TRE; adenoviral propagation;
KW death protein; tumour; ss.
XX
OS Mastadenovirus.
XX
XX Key Location/Qualifiers
FH CDS 2..307
FT /*tag= a
FT /product= "death protein"
XX
XX WO200015820-A1.
XX
XX 23-MAR-2000.
XX
XX 10-SEP-1999; 99WO-US020718.
XX
XX 10-SEP-1998; 98US-0099791P.
XX
XX 09-SEP-1999; 99US-00392822.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu DC, Henderson DR;
XX
XX WPI; 2000-271456/23.
XX
XX P-PSDB; AAY84407.
XX
XX Adenovirus vectors comprising cell-status specific response elements
XX useful in gene therapy protocols for the treatment of cancers.
XX
XX Disclosure; Fig 9; 79pp; English.
XX
XX The present sequence encodes an adenoviral death protein, which is used
XX to construct the vectors of the invention. The specification describes
XX adenoviral vectors which comprise an adenovirus gene under
XX transcriptional control of a cell status specific transcriptional
XX regulatory element (TRE). The TRE is preferably one that is essential for
XX adenoviral propagation. The adenovirus vectors may be used for the
XX treatment of a range of tumours such as lung, stomach, breast, colon and
XX rectum, and uterine and cervix cancers
XX
XX Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 307; DB 3; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GATCACCAGTCAACCATCGGCCCAACACGACTATCGCAACACCACTGCTACCGACT 60
Db |||||||
QY 1 GATCACCAGTCAACCATCGGCCCAACACGACTATCGCAACCACTGCTACCGACT 60
Db |||||||
QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTCTTGTCAATGACTGGCGAGCTTGGA 120
Db |||||||
```

```
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTCTTGTCAATGACTGGCGAGCTTGGA 120
QY 121 CATGTGGTGGTTTCCCATAGCGCTTATGTTTGGCTTATTATTATGCGCTTATTG 180
Db |||||||
QY 121 CATGTGGTGGTTTCCCATAGCGCTTATGTTTGGCTTATTATTATGCGCTTATTG 180
Db |||||||
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCGCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db |||||||
QY 181 TTGCCTAAAGCGCAGACGCGCCAGACCCGCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db |||||||
QY 241 ACACATGAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
Db |||||||
QY 241 ACACATGAAATTCATAGATTGGACGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
Db |||||||
QY 301 TGATTAA 307
Db |||||||
QY 301 TGATTAA 307
Db |||||||

RESULT 6
AAI70186
ID AAI70186 standard; DNA; 307 BP.
XX
AC AAI70186;
XX
DT 11-SEP-2003 (revised)
DT 07-JAN-2002 (first entry)
XX
DE Adenovirus death protein gene.
XX
DE WO2000172994-A2.
XX
XX Human adenovirus type 2.
XX
XX Key Location/Qualifiers
FH CDS 2..307
FT /*tag= a
XX
XX WO2000172994-A2.
XX
XX 04-OCT-2001.
XX
XX 21-MAR-2001; 2001WO-US009224.
XX
XX 24-MAR-2000; 2000US-0191861P.
XX
XX (CALY-) CALYDON INC.
XX
XX Yu D, Zhang H, Henderson DR;
XX
XX WPI; 2001-639229/73.
XX
XX P-PSDB; AAM50206.
XX
XX Human urothelial cell specific uroplakin transcriptional regulatory
XX sequences, useful for producing adenoviral vectors which can be used to
XX confer selective cytotoxicity to target cells, especially bladder cancer
XX cells.
XX
XX Example 6; Fig 12; 147pp; English.
XX
XX The present sequence is that of the coding region of the adenovirus death
XX protein. The sequence was obtained by PCR amplification and used in the
XX construction of adenoviral vectors in which ADP expression and used in the
XX control of a urothelial cell-specific transcriptional regulatory element
XX (TRE) derived from the human uroplakin II gene 5' flanking region (see
XX AAI70144). This is an example of adenoviral vectors of the invention.
XX Such vectors comprise a gene, preferably an adenovirus gene, under
XX transcriptional control of a urothelial cell-specific TRE. They display
XX urothelial cell-specific cytotoxicity, and are used for the specific,
XX targeted gene therapy of bladder cancer. (Updated on 11-SEP-2003 to
XX standardise OS field)
```



```
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match      100.0%; Score 307; DB 4; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACGGCTCAACCATCGCGCCCAACGCGACTATCGCAACACCACTGCTACCGGACT 60
DB 1 GATGACGGCTCAACCATCGCGCCCAACGCGACTATCGCAACACCACTGCTACCGGACT 60

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120

QY 121 CATGTGTGTTTCCATAGCGCTTATGTTTGTGCTTATTTATATGAGGCTTATTG 180
DB 121 CATGTGTGTTTCCATAGCGCTTATGTTTGTGCTTATTTATATGAGGCTTATTG 180

QY 181 TTGCCTAAAGCGCAGACGGCCGACACCCCATCTATAGCCCTATCATTTGCTCAACCC 240
DB 181 TTGCCTAAAGCGCAGACGGCCGACACCCCATCTATAGCCCTATCATTTGCTCAACCC 240

QY 241 ACACATGAAATAATTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300
DB 241 ACACATGAAATAATTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307
DB 301 TGATTAA 307

RESULT 7
AAH43535
ID AAH43535 standard; cDNA; 307 BP.
AC AAH43535;
XX
DT 11-SEP-2003 (revised)
DT 07-JAN-2002 (first entry)
DE ADP nucleotide sequence.
XX
KW Adenovirus; ADP; replication-competent; adenoviral vector; TRE;
KW transcriptional regulatory element; mutation; deletion; IRES; promoter;
KW internal ribosome entry site; cytotoxic; cancer; bladder; ss.
XX
OS unidentified adenovirus.
XX
FH Key Location/Qualifiers
FT CDS 2..307
FT /*tag= a
FT /product= "ADP"
XX
PN WC200173093-A2.
XX
PD 04-OCT-2001.
XX
PF 21-MAR-2001; 2001WO-US009036.
XX
PR 24-MAR-2000; 2000US-0192156P.
XX
PA (CALY-) CALYDON INC.
XX
PI Yu D, Li Y, Henderson DR;
XX
XX WPI; 2001-639234/73.
DR P-PSDB; AAB47591.
XX
PT Replication-competent adenoviral vector, useful e.g. for killing cancer
PT cells, contains two genes linked by internal ribosome entry site and
PT controlled by target-specific regulator.
XX
```

PS Disclosure; Fig 9; 148pp; English.

XX This sequence encodes adenoviral ADP. This coding sequence may be used in the replication-competent adenoviral vector (A) of the invention which contains two genes (G1, G2) that are co-transcribed as a single mRNA and under control of a heterologous, target cell-specific transcriptional regulatory element (TRE). G2 has a mutation in, or deletion of, its endogenous promoter and is controlled from an internal ribosome entry site (IRES). The ADP coding sequence may be used as G1 or G2. (A) has greater specificity for a target cell than a similar vector in which TRE is operably linked to a gene and which lacks an IRES. (A) are used to modify the genotype of target cells, optionally in vitro with subsequent return of altered cells to the host and where G2 is a cytotoxic gene, to confer selective cytotoxicity to target cells, especially for killing cancer cells. ADP displays a cytotoxic, particularly cell lysis, function. Also (A) are used for diagnosis and monitoring, e.g. detection of bladder cancer cells. The target cell-specific TRE ensures that (A) has better targeting specificity, with minimal replication in non-target cells, so a runaway infection is prevented but production of adenoviral proteins in target cells activates and/or stimulates the immune response against target cells producing such proteins. The use of an IRES (rather than two identical control elements) eliminates the risk of homologous recombination and may provide enough extra space for an additional (therapeutic) gene. (Updated on 11-SEP-2003 to standardise OS field)

XX Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 307; DB 5; Length 307; Best Local Similarity 100.0%; Pred. No. 2.4e-94; Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GATGACGGCTCAACCATCGCGCCCAACGCGACTATCGCAACACCACTGCTACCGGACT 60

DB 1 GATGACGGCTCAACCATCGCGCCCAACGCGACTATCGCAACACCACTGCTACCGGACT 60

QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120

DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120

QY 121 CATGTGTGTTTCCATAGCGCTTATGTTTGTGCTTATTTATATGAGGCTTATTG 180

DB 121 CATGTGTGTTTCCATAGCGCTTATGTTTGTGCTTATTTATATGAGGCTTATTG 180

QY 181 TTGCCTAAAGCGCAGACGGCCGACACCCCATCTATAGCCCTATCATTTGCTCAACCC 240

DB 181 TTGCCTAAAGCGCAGACGGCCGACACCCCATCTATAGCCCTATCATTTGCTCAACCC 240

QY 241 ACACATGAAATAATTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300

DB 241 ACACATGAAATAATTCATAGATTGACGCTCTGAAACCAATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307

DB 301 TGATTAA 307

RESULT 8

ABK99587

ID ABK99587 standard; DNA; 307 BP.

XX

AC ABK99587;

XX

DT 21-OCT-2002 (first entry)

XX

DE DNA encoding adenovirus death protein (ADP).

XX

XX Adenovirus; transcriptional regulatory element; TRE; prostate; liver; breast cancer; colon cancer; antitumor; gene; ds; probasin; PB; human; rat; carcinoembryonic antigen; prostate-specific antigen; ADP; adenovirus death protein; glandular kallikrein.

XX

XX Unidentified.

OS

PN US2002068049-A1.  
XX 06-JUN-2002.  
XX 06-DEC-2000; 2000US-00732169.  
XX 10-SEP-1998; 98US-00151376.  
XX (HEND/) HENDERSON D R.  
XX (SCHU/) SCHUUR E R.  
XX Henderson DR, Schuur ER;  
XX WPI: 2002-582468/62.  
XX P-PSDB; ABG69353.  
XX Novel adenovirus vector comprises adenovirus gene under transcriptional control of cell-type specific transcriptional response element for conferring selective toxicity on target cell and for suppressing tumor growth.  
XX Disclosure; Fig 19; 83pp; English.  
XX The invention relates to an adenovirus vector (AV) comprising an AV gene under transcriptional control of a cell type-specific transcriptional regulatory element (TRE) and optionally a first AV gene under control of a first cell type-specific TRE and a second gene under control of a second cell type-specific TRE, where the first and second cell type-specific TREs are substantially identical. When the vector is introduced into a cell (e.g. prostate cell, liver cell, breast cancer cell or colon cancer cell) it allows the cell type-specific TRE to function, resulting in cytotoxicity. The vector is useful for suppressing tumour growth of a target cell. This sequence represents a polynucleotide used in the scope of the invention  
XX  
XX SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;  
Query Match 100.0%; Score 307; DB 6; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.4e-94;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACACCACTGCTACCGGACT 60  
Db 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACACCACTGCTACCGGACT 60  
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
Qy 121 CATGTGTGGTGTTCATAGGCTTATGTTTGTGCTTATTTATGCTTATTTG 180  
Db 121 CATGTGTGGTGTTCATAGGCTTATGTTTGTGCTTATTTATGCTTATTTG 180  
Qy 181 TTGCTTAAGCGCAGACGCGCAGACCCCATCTATAGGCTTATGCTTCAACCC 240  
Db 181 TTGCTTAAGCGCAGACGCGCAGACCCCATCTATAGGCTTATGCTTCAACCC 240  
Qy 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300  
Db 241 ACACAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300  
Qy 301 TGATTAA 307  
Db 301 TGATTAA 307  
RESULT 9  
ACD07312  
ID ACD07312 standard; DNA; 307 BP.  
XX  
XX ACD07312;  
XX  
XX DT 27-OCT-2003 (revised)  
DT 07-AUG-2003 (first entry)  
XX DNA encoding adenovirus death protein (ADP).  
XX Adenoviral vector; adenovirus gene; transcriptional control; TRE; cell type-specific; transcriptional response element; PSA; hKlK; prostate-specific antigen; glandular kallikrein; probastin; PB; carcinoembryonic antigen; CEA; mucin-like glycoprotein DF3; MUC1; cytotoxicity; neoplasia; tumour growth; gene therapy; cytostatic; adenovirus death protein; ADP; gene; ds.  
XX unidentified adenovirus.  
XX US2003044383-A1.  
XX 06-MAR-2003.  
XX 10-SEP-1998; 98US-00151376.  
XX 27-JUN-1995; 95US-00495034.  
XX 20-AUG-1996; 96US-00699753.  
XX 03-MAR-1997; 97US-0039597P.  
XX 03-MAR-1997; 97US-0039599P.  
XX 03-MAR-1997; 97US-0039762P.  
XX 03-MAR-1997; 97US-0039763P.  
XX 02-MAR-1998; 98US-00033333.  
XX 02-MAR-1998; 98US-00033428.  
XX 02-MAR-1998; 98US-00033555.  
XX (HEND/) HENDERSON D R.  
XX (SCHU/) SCHUUR E R.  
XX Henderson DR, Schuur ER;  
XX WPI: 2003-456547/43.  
XX P-PSDB; ABU10308.  
XX New adenovirus vector for transfecting target host cells, comprises an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element.  
XX Disclosure; Fig 19; 83pp; English.  
XX The present invention relates to adenoviral vectors comprising an adenovirus gene under transcriptional control of a cell type-specific transcriptional response element (TRE). Example TREs given in the specification include human prostate-specific antigen (PSA) TRE, human glandular kallikrein (hKlK) TRE, rat probastin (PB) TRE, human carcinoembryonic antigen (CEA) TRE, and human mucin-like glycoprotein DF3 (MUC1) TRE. The modified adenovirus vector is useful as a vehicle for introducing new genetic capability, particularly associated with cytotoxicity for treating neoplasia. For example, the vector may be used in a target cell to suppress tumour growth, or to kill the target cell. The vector is particularly useful in gene therapy. The present sequence encodes adenovirus death protein (ADP). (Updated on 27-OCT-2003 to standardise OS field)  
XX  
XX SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;  
Query Match 100.0%; Score 307; DB 8; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.4e-94;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACACCACTGCTACCGGACT 60  
Db 1 GATGACCGGCTCAACCATCGCGCCCAACAGCGACTATCGCAACACCACTGCTACCGGACT 60  
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
Qy 121 CATGTGTGGTGTTCATAGGCTTATGTTTGTGCTTATTTATGCTTATTTG 180

```
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGCGCTTATTG 180
Qy 181 TTGCTTAAAGCGGAGAGCGGCCAGACCCCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCTTAAAGCGGAGAGCGGCCAGACCCCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Qy 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 10
AD136397
ID AD136397 standard; DNA; 307 BP.
XX
AC AD136397;
XX
DT 22-APR-2004 (first entry)
XX
DE Human mucin (MUC1) transcriptional response element DNA SeqID61.
XX
KW ds; mucin; MUC1; human; prostate; transcriptional response element; TRE;
KW polyethylene glycol; PEG; masking agent; tumour cell growth;
KW proliferation; psoriatic lesion; wound healing; hyperplasia; cancer;
KW cytotatic; antipsoriatic; vulnery; human.
XX
OS Homo sapiens.
XX
PN US2003152553-A1.
XX
PD 14-AUG-2003.
XX
PF 02-MAY-2002; 2002US-00139089.
XX
PR 27-JUN-1995; 95US-00495034.
PR 26-JUN-1996; 96US-00669753.
PR 03-MAR-1997; 97US-0039597P.
PR 03-MAR-1997; 97US-0039762P.
PR 03-MAR-1997; 97US-0039763P.
PR 02-MAR-1998; 98US-00033333.
PR 02-MAR-1998; 98US-00033428.
PR 02-MAR-1998; 98US-00033555.
PR 10-SEP-1998; 98US-00151376.
PR 02-JUN-2000; 2000US-00509591.
XX
PA (LITV/) LITTLE A S.
PA (LAMP/) LAMPARSKI H G.
PA (HEND/) HENDERSON D R.
PA (SCHU/) SCHUUR E R.
XX
PI Little AS, Lamparski HG, Henderson DR, Schuur ER;
XX
XX WPI; 2004-119002/12.
XX
XX Composition comprising replication competent adenovirus having adenovirus
XX gene essential for replication under transcriptional control of cell type
XX specific transcriptional response element and masking agent.
XX
XX Example 5; SEQ ID NO 61; 115pp; English.
XX
XX This invention relates to a novel composition that contains a replication
XX competent adenovirus capable of transfecting target host cells.
XX Specifically, it comprises an adenoviral gene essential for replication
XX (E1A, E1B or E4), which is under the transcriptional control of a
XX prostate specific transcriptional response element (TRE) and polyethylene
XX glycol (PEG) as the masking agent. The present invention describes this
XX composition as useful for suppressing tumour cell growth and for lowering
XX the levels of tumour cell markers. It can also be used for introducing
XX transient expression that may be involved in treating undesired
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CC proliferations other than tumours, such as psoriatic lesions and wound
CC healing. In addition, it is useful for detecting cells where a cell type-
CC specific TRE is functional in a biological sample and for treating
CC prostate-associated diseases such as hyperplasia and cancer. As such,
CC these compositions exhibit cytostatic, antipsoriatic and vulnery
CC activities. This polynucleotide sequence is the human mucin (MUC1) TRE
CC DNA sequence of the invention. NOTE: This sequence is identical to that
CC given as SeqID 10.
XX
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 12; Length 307;
Best Local Similarity 100.0%; Pred. No. 2.4e-94;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GATGACCGGCTCAACCATCGCGCCCAACCGGACTATCGCAACACCACTCTCTACCGACT 60
Db 1 GATGACCGGCTCAACCATCGCGCCCAACCGGACTATCGCAACACCACTCTCTACCGACT 60
Qy 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
Db 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120
Qy 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGCGCTTATTG 180
Db 121 CATGTGGTGGTTTCCATAGCGCTTATGTTGTTGGCTTATTATTATGCGCTTATTG 180
Qy 181 TTGCTTAAAGCGGAGAGCGGCCAGACCCCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Db 181 TTGCTTAAAGCGGAGAGCGGCCAGACCCCCCATCTATAGCCCTATCATTTGCTCAACCC 240
Qy 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Db 241 ACACATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA 300
Qy 301 TGATTAA 307
Db 301 TGATTAA 307

RESULT 11
AD136417
ID AD136417 standard; DNA; 307 BP.
XX
AC AD136417;
XX
DT 22-APR-2004 (first entry)
XX
DE DNA encoding the human ADP protein SeqID10.
XX
KW ds; gene; human ; prostate; transcriptional response element; TRE;
KW polyethylene glycol; PEG; masking agent; tumour cell growth;
KW proliferation; psoriatic lesion; wound healing; hyperplasia; cancer;
KW cytotatic; antipsoriatic; vulnery; ADP.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 2..307
XX FT /*tag= a
XX FT /product= "ADP protein"
XX
XX US2003152553-A1.
XX
XX 14-AUG-2003.
XX
XX 02-MAY-2002; 2002US-00139089.
XX
XX 27-JUN-1995; 95US-00495034.
XX 26-JUN-1996; 96US-00669753.
XX 03-MAR-1997; 97US-0039597P.
XX 03-MAR-1997; 97US-0039762P.
XX 03-MAR-1997; 97US-0039763P.
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PR 02-MAR-1998; 98US-00033333.  
 PR 02-MAR-1998; 98US-00033428.  
 PR 02-MAR-1998; 98US-00033555.  
 PR 10-SEP-1998; 98US-00151376.  
 PR 02-JUN-2000; 2000US-00509591.  
 XX (LITT//) LITTLE A S.  
 PA (LAMP//) LAMPARSKI H G.  
 PA (HEND//) HENDERSON D R.  
 PA (SCHU//) SCHUUR E R.  
 XX  
 PI Little AS, Lamparski HG, Henderson DR, Schuur ER;  
 XX  
 DR WPI; 2004-119002/12.  
 DR P-PSDB; ADI36347.  
 XX  
 XX Composition comprising replication competent adenovirus having adenovirus  
 PT gene essential for replication under transcriptional control of cell type  
 PT specific transcriptional response element and masking agent.  
 XX  
 XX Disclosure; SEQ ID NO 10; 115pp; English.  
 XX  
 CC This invention relates to a novel composition that contains a replication  
 CC competent adenovirus capable of transfecting target host cells.  
 CC Specifically, it comprises an adenoviral gene essential for replication  
 CC (E1A, E1B or E4), which is under the transcriptional control of a  
 CC prostate specific transcriptional response element (TRE) and polyethylene  
 CC glycol (PEG) as the masking agent. The present invention describes this  
 CC composition as useful for suppressing tumour cell growth and for lowering  
 CC the levels of tumour cell markers. It can also be used for introducing  
 CC transient expression that may be involved in treating undesired  
 CC proliferations other than tumours, such as psoriatic lesions and wound  
 CC healing. In addition, it is useful for detecting cells where a cell type-  
 CC specific TRE is functional in a biological sample and for treating  
 CC prostate-associated diseases such as hyperplasia and cancer. As such,  
 CC these compositions exhibit cytostatic, antiproliferative and vulnerary  
 CC activities. This polynucleotide sequence is the DNA encoding the human  
 CC ADP protein of the invention. NOTE: This sequence is identical to that  
 CC given as SeqID 61.  
 XX  
 XX Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 12; Length 307;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-94;  
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GATGACCGGCTCAACCATCGCGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60  
 DB 1 GATGACCGGCTCAACCATCGCGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60  
 QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
 DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
 QY 121 CATGTGGTGGTTCATAGATTGGAGCGGCTTATGTTGGCTTTATTATTATGTCGCTTATTG 180  
 DB 121 CATGTGGTGGTTCATAGATTGGAGCGGCTTATGTTGGCTTTATTATTATGTCGCTTATTG 180  
 QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240  
 DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240  
 QY 241 ACACAATGAAAAAATTCATAGATTGGAGCGGCTTATGTTGGCTTTATTATTATGTCGCTTATTG 300  
 DB 241 ACACAATGAAAAAATTCATAGATTGGAGCGGCTTATGTTGGCTTTATTATTATGTCGCTTATTG 300  
 QY 301 TGATTAA 307  
 DB 301 TGATTAA 307

RESULT 12  
 ADV21029

ID ADV21029 standard; DNA; 307 BP.  
 XX  
 AC ADV21029;  
 XX  
 DT 24-FEB-2005 (first entry)  
 XX  
 DE Human mucin like glycoprotein DF3 (MUC1) TRE DNA.  
 XX  
 DE Vector; gene transfer; cloning vehicle; genetic engineering;  
 KW prostate cancer; gene therapy; vaccine; cytostatic; TRE;  
 KW transcriptional regulatory element; PSE; prostate specific enhancer; PSA;  
 KW prostate specific antigen; cancer; ds; mucin like glycoprotein DF3; MUC1.  
 XX  
 OS Homo sapiens.  
 XX  
 XX US2004241857-A1.  
 XX  
 PD 02-DEC-2004.  
 XX  
 PF 13-APR-2004; 2004US-00822873.  
 XX  
 XX 27-JUN-1995; 95US-00495034.  
 PR 28-JUN-1996; 96US-00669753.  
 PR 10-SEP-1998; 98US-00151376.  
 PR 06-DEC-2000; 2000US-00732169.  
 XX  
 PA (HEND//) HENDERSON D R.  
 PA (SCHU//) SCHUUR E R.  
 XX  
 PI Henderson DR, Schuur ER;  
 XX  
 DR WPI; 2005-011642/01.  
 XX  
 XX New adenovirus vector comprising an adenovirus early gene essential for  
 PT propagation under the control of a human prostate specific antigen  
 PT promoter and a human prostate specific antigen enhancer, for treating  
 PT prostate cancer.  
 XX  
 XX Example 5; SEQ ID NO 61; 112pp; English.  
 XX  
 CC The present invention relates to an adenovirus vector comprising an  
 CC adenovirus early gene essential for propagation under the control of a  
 CC human prostate specific antigen promoter and a human prostate specific  
 CC antigen (PSA) enhancer. The invention is useful for treating a patient  
 CC suffering from prostate cancer and for making mammalian hosts that are  
 CC transiently transgenic and for detecting the presence of cells that  
 CC permit the function of a cell type-specific transcriptional regulatory  
 CC element (TRE) in a sample. The invention is also used in the gene therapy  
 CC and also as vaccine. The present sequence is the human mucin like  
 CC glycoprotein DF3 (MUC1) TRE DNA. This sequence is used to construct  
 CC replication competent prostate-specific attenuated adenoviruses.

Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 307; DB 14; Length 307;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-94;  
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GATGACCGGCTCAACCATCGCGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60  
 DB 1 GATGACCGGCTCAACCATCGCGCCCAACGAGACTATCGCAACACCACTGCTACCGGACT 60  
 QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
 DB 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
 QY 121 CATGTGGTGGTTCATAGATTGGAGCGGCTTATGTTGGCTTTATTATTATGTCGCTTATTG 180  
 DB 121 CATGTGGTGGTTCATAGATTGGAGCGGCTTATGTTGGCTTTATTATTATGTCGCTTATTG 180  
 QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240  
 DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGGCTTATCATTTGCTCAACCC 240

QY 241 ACACAAATGAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTTCTTTTACAGTA 300  
DB 241 ACACAAATGAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTTCTTTTACAGTA 300  
QY 301 TGATTAA 307  
DB 301 TGATTAA 307  
RESULT 13  
ADV20978  
ID ADV20978 standard; DNA; 307 BP.  
XX  
AC ADV20978;  
DT 24-FEB-2005 (first entry)  
DE Adenovirus death protein (ADP) encoding DNA.  
XX  
KW Vector; gene transfer; cloning vehicle; genetic engineering;  
KW prostate cancer; gene therapy; vaccine; cytostatic;  
KW prostate-specific antigen; TRE; transcriptional regulatory element; PSE;  
KW prostate specific enhancer; PSA; prostate specific antigen; cancer; ds;  
KW ADP; adenovirus death protein; gene.  
XX  
OS unidentified adenovirus.  
XX  
FH Key Location/Qualifiers  
FT CDS 2..307  
FT /\*tag= a  
FT /product= "Adenovirus death protein (ADP) "  
XX  
PN US2004241857-A1.  
XX  
PD 02-DEC-2004.  
XX  
PF 13-APR-2004; 2004US-00822873.  
XX  
XX 27-JUN-1995; 95US-00495034.  
PR 26-JUN-1996; 96US-00669753.  
PR 10-SEP-1998; 98US-00151376.  
PR 06-DEC-2000; 2000US-00732169.  
XX  
XX (HEND/) HENDERSON D R.  
PA (SCHU/) SCHUUR E R.  
XX  
XX Henderson DR, Schuur ER;  
XX WPI; 2005-011642/01.  
XX  
XX New adenovirus vector comprising an adenovirus early gene essential for  
PT propagation under the control of a human prostate specific antigen  
PT promoter and a human prostate specific antigen enhancer, for treating  
PT prostate cancer.  
XX  
XX Disclosure; SEQ ID NO 10; 112pp; English.  
XX  
XX The present invention relates to an adenovirus vector comprising an  
CC adenovirus early gene essential for propagation under the control of a  
CC human prostate specific antigen promoter and a human prostate specific  
CC antigen (PSA) enhancer. The invention is useful for treating a patient  
CC suffering from prostate cancer and for making mammalian hosts that are  
CC transiently transgenic and for detecting the presence of cells that  
CC permit the function of a cell type-specific transcriptional regulatory  
CC element (TRE) in a sample. The invention is also used in the gene therapy  
CC and also as vaccine. The present sequence is the adenovirus death protein  
CC encoding DNA.  
XX  
SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;  
Query Match 100.0%; Score 307; DB 14; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.4e-94;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GATGACCGGCTCAACCATCGCGCCCAACGGAATATCGCAACACCACTGCTACCGACT 60  
DB 1 GATGACCGGCTCAACCATCGCGCCCAACGGAATATCGCAACACCACTGCTACCGACT 60  
QY 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
DB 61 AACATCTGCCCTAAATTTTACCCCAAGTTTCATGCTTTGTCAATGACTGGGCGAGCTTGA 120  
QY 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGGCTTATTATTATGTCGCTTATTTG 180  
DB 121 CATGTGGTGGTTTTCATAGCGCTTATGTTTGGCTTATTATTATGTCGCTTATTTG 180  
QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGCCCTATCATTTGCTCAACCC 240  
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCACTATAGCCCTATCATTTGCTCAACCC 240  
QY 241 ACACAAATGAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTTCTTTTACAGTA 300  
DB 241 ACACAAATGAAAAATTCATAGATTGACGGTCTGAAACCATGTTCTTCTTTTACAGTA 300  
QY 301 TGATTAA 307  
DB 301 TGATTAA 307  
RESULT 14  
ADM47774  
ID ADM47774 standard; DNA; 307 BP.  
XX ADM47774;  
XX 07-APR-2005 (first entry)  
DE Adenovirus death protein coding sequence.  
XX  
KW Gene therapy; vector; prostate tumor; cytostatic; vasotropic; vulnerary;  
KW antipsoriatic; antimicrobial; immunomodulator; gene; ds.  
XX  
OS Human adenovirus type 2.  
XX  
FH Key Location/Qualifiers  
FT CDS 2..307  
FT /\*tag= a  
FT /product= "Adenovirus death protein"  
XX  
XX WO2005007832-A2.  
XX  
XX 27-JAN-2005.  
XX  
XX 24-FEB-2004; 2004WO-US005518.  
XX  
XX 24-FEB-2003; 2003US-0450232P.  
XX  
XX (CELL-) CELL GENESYS INC.  
XX  
XX Harding T, Yu DC;  
XX  
XX WPI; 2005-102098/11.  
XX P-PSDB; ADM47775.  
XX  
XX New replication competent adenovirus vector comprising an inducible  
PT transcriptional transactivator coding sequence and an adenovirus gene,  
PT useful for treating cancer, psoriatic lesions, restenosis or wound  
PT healing.  
XX  
XX Disclosure; SEQ ID NO 10; 66pp; English.  
XX  
XX The present sequence is the coding sequence for adenovirus death protein  
CC (ADP). A claimed replication competent adenovirus vector comprises: an  
CC inducible transcriptional transactivator (Tt) coding sequence under the  
CC transcriptional control of a cell type-specific TRE (Ct-TRE); and an

adenovirus gene under transcriptional control of a TRE regulated by the TT, where the TT is functionally responsive to an exogenous inducer agent. The adenovirus gene is preferably a gene essential for adenoviral replication. The TT may be inhibited or activated by the inducing agent. Also claimed is an adenovirus vector comprising: an inducible TT coding sequence under the transcriptional control of a CT-TRE; and an adenovirus gene under transcriptional control of a TRE regulated by the TT and a second gene under transcriptional control of a second TRE, where the TT is activated by an exogenous inducing agent. The second gene may be an adenoviral gene essential for adenovirus replication, or a transgene such as a cytotoxic gene. One embodiment of the invention provides adenovirus vectors in which an adenovirus gene is under transcriptional control of a first transactivated regulated TRE and a polynucleotide encoding an ADP under control of a second transactivator regulated TRE, where the adenovirus gene is essential for replication. Also claimed are host cells comprising the replication competent adenovirus vector, and methods for propagating and regulating the vector. A claimed method for selective cytolysis of a target tumor cell line involves introducing the adenovirus vector into a cell which allows the CT-TRE to function, and administering an inducing agent such that the adenovirus vector is propagated and causes lysis of target prostate cells. The adenovirus vector can also be used to treat prostatic lesions, restenosis, wound healing, tissue repair, enhanced immune response, resistance to infection, production of factors, enhanced proliferation, investigation of metabolic or other physiological pathways, or comparison of activity of cells in the presence and absence of the virus introduced transgene. In vectors of the invention, expression of a viral gene essential for replication is regulated both by the CT-TRE and the transactivator regulated TRE, and indirectly by the concentration of the inducing agent.

XX SQ Sequence 307 BP; 77 A; 82 C; 59 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 14; Length 307;  
Best Local Similarity 100.0%; Pred. No. 2.4e-94;  
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 240  
DB 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 240

QY 241 ACACAATGAAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTTTTACAGTA 300  
DB 241 ACACAATGAAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300

QY 301 TGATTAA 307  
DB 301 TGATTAA 307

RESULT 15

ADW28317

ID ADW28317 standard; DNA; 917 BP.

XX AC

ADW28317;

XX XX

07-APR-2005 (first entry)

DE DT

Partial DNA sequence of Ad5-yCD/mutTK(SR39)rep-ADP virus (E3 region).

XX KW

chemotherapy; cytosine deaminase; SR39; herpes simplex virus type 1; thymidine kinase; death protein gene; cancer; neoplasia; 5-fluorocytosine;

ganciclovir; Ad5-yCD/mutTK(SR39)rep-ADP; ss.

OS Human adenovirus type 5.

OS Synthetic.

XX WO2005007109-A2.

PN 27-JAN-2005.

XX 09-JUL-2004; 2004WO-US022320.

XX 09-JUL-2003; 2003US-0486219P.

PR (FORD-) FORD HEALTH SYSTEM HENRY.

XX Freytag SD, Kim JH, Barton K, Paielli D;

XX WPI; 2005-101983/11.

XX Novel isolated polynucleotide comprising nucleotide sequence of yeast

PT cytosine deaminase/mutant SR 39 herpes simplex virus type 1 thymidine

PT kinase fusion gene, useful for treating mammalian patient having

PT malignancy or solid tumor.

XX Example; SEQ ID NO 3; 62pp; English.

XX The specification describes a polynucleotide comprising a nucleotide

CC sequence of yeast cytosine deaminase/mutant SR39 herpes simplex virus

CC type 1 thymidine kinase fusion gene, and further comprising an adenovirus

CC type 5 adenovirus death protein gene. The polynucleotide of the invention

CC limits the side effects of cancer treatment by using only lower doses of

CC radiation. The polypeptide encoded by the above polynucleotide is useful

CC for converting 5-fluorocytosine or ganciclovir into active

CC chemotherapeutic agents. Pharmaceutical compositions comprising

CC recombinant adenoviruses comprising polynucleotides of the invention are

CC useful for treating a mammalian patient having a malignancy or solid

CC tumor. The present sequence represents a partial sequence (the E3 region)

CC of a recombinant adenovirus comprising the polynucleotide of the

CC invention. The recombinant adenovirus is designated Ad5-

CC yCD/mutTK(SR39)rep-ADP.

XX SQ Sequence 917 BP; 236 A; 223 C; 194 G; 264 T; 0 U; 0 Other;

Query Match 100.0%; Score 307; DB 14; Length 917;

Best Local Similarity 100.0%; Pred. No. 4.1e-94;

Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGGGA 120

DB 482 AACATCTGCCCTAAATTTACCCCAAGTTTCATGCTTTGTCAATGACTGGCGAGCTTGGGA 541

QY 121 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGCTTATTTATTTATGCGCTTATTTG 180

DB 542 CATGTGGTGGTTTTCCATAGCGCTTATGTTTGGCTTATTTATTTATGCGCTTATTTG 601

QY 181 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 240

DB 602 TTGCTTAAAGCGCAGACGCGCCAGACCCCATCTATAGGCTTATCATTTGTGCTCAACCC 661

QY 241 ACACAATGAAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 300

DB 662 ACACAATGAAAAAATTCATAGATTGGAGCGGTCTGAAACCAATGTTCTCTCTTTTACAGTA 721

QY 301 TGATTAA 307

DB 722 TGATTAA 728

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Job time : 477 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: gb\_env.\*  
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7: gb\_ph.\*  
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9: gb\_ro.\*  
10: gb\_sts.\*  
11: gb\_sy.\*  
12: gb\_un.\*  
13: gb\_vi.\*  
14: gb\_htgs.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	307	100.0	307	6	AR137114 Sequence
2	307	100.0	307	6	AR160082 Sequence
3	307	100.0	307	6	BD070679 Adenoviru
4	307	100.0	307	6	BD195488 Adenoviru
5	307	100.0	307	6	BD195538 Adenoviru
6	307	100.0	307	6	BD217928 Adenoviru
7	307	100.0	307	6	BD224262 Adenoviru
8	307	100.0	307	6	AR223335 Sequence
9	307	100.0	307	6	AR349303 Sequence
10	307	100.0	307	6	AR451690 Sequence
11	307	100.0	307	6	AR451740 Sequence
12	307	100.0	307	6	AR474487 Sequence
13	307	100.0	307	6	AR635125 Sequence
14	307	100.0	307	6	AR669908 Sequence
15	307	100.0	3454	13	HAD293912 Human ade
16	307	100.0	3454	13	HAD293914 Human ade
17	307	100.0	3454	13	HAD293916 Human ade
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	22	305.4	99.5	3454	13	HAD293915	AJ293915 Human ade
	23	303.8	99.0	34427	6	AR651085	AR651085 Sequence
	24	302.2	98.4	2019	13	ADV16037	Y16037 Adenovirus
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	31	196	63.8	33699	6	AX084506	AX084506 Sequence
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	33	196	63.8	34341	6	AX084505	AX084505 Sequence
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	38	196	63.8	35724	6	AX084516	AX084516 Sequence
	39	196	63.8	35871	6	AR403724	AX084516 Sequence
	40	196	63.8	35934	13	AV339865	AX083724 Sequence
	41	196	63.8	35935	6	AR091533	AY339865 Human ade
	42	196	63.8	35935	6	AR102226	AR091533 Sequence
	43	196	63.8	35935	6	AR116313	AR102226 Sequence
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ALIGNMENTS

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ACCESSION	AR137114.1	GI:14478623				
VERSION						
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 307)					
AUTHORS	Henderson,D.R., Schuur,E.R. and Yu,D.-C.					
TITLE	Adenovirus vectors specific for cells expressing androgen receptor and methods of use thereof					
JOURNAL	Patent: US 6197293-A 21.06-MAR-2001;					
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Qy	121	CATGCGGTGGTTCATGCGGCTTATGTTTGGCTTATTTATGTCGCTTATTTG	180		
Db	121	CATGCGGTGGTTCATGCGGCTTATGTTTGGCTTATTTATGTCGCTTATTTG	180		
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Db	181	TTGCGCTAAAGCGCAGACGCGCCAGACCCCACTATAGCCTCATCTGTCGTCAACCC	240		

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LOCUS BD070679 307 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 22 from patent US 6254862.
ACCESSION AR160082
VERSION AR160082.1 GI:16223671
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 307)
Little,A.S., Henderson,D.R., Schuur,E.R. and Lamparski,H.
AUTHORS Adenovirus vectors specific for cells expressing alpha-fetoprotein
TITLE and methods of use thereof
JOURNAL Patent: US 6254862-A 22 03-JUL-2001;
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Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||||
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LOCUS BD070679 307 bp DNA linear PAT 27-AUG-2002
DEFINITION Adenovirus vectors specific for cells expressing androgen receptor
and methods of use thereof.
ACCESSION BD070679
VERSION BD070679.1 GI:22616282
KEYWORDS JP 2001515351-A/21.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 307)
Yu,D.C., Henderson,D.R., Schuur,E.R. and Lamparski,H.G.
AUTHORS Adenovirus vectors specific for cells expressing androgen receptor
TITLE and methods of use thereof.

Qy 241 ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTTTTACAGTA 300
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RESULT 4
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LOCUS BD195488 307 bp DNA linear PAT 17-JUL-2003
DEFINITION Adenovirus vectors containing heterologous transcription regulatory
elements and methods of using same.
ACCESSION BD195488
VERSION BD195488.1 GI:33005258
KEYWORDS JP 2002514074-A/9.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 307)
Henderson,D.R., Yu,D.C. and Lamparski,H.G.
AUTHORS Adenovirus vectors containing heterologous transcription regulatory
TITLE elements and methods of using same
JOURNAL Patent: JP 2002514074-A 9 14-MAY-2002;
COMMENT
OS Unidentified
PN JP 2002514074-A/9
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Patent: JP 2001515351-A 21 18-SEP-2001;
CALYDON INC
COMMENT OS Unidentified
PN JP 2001515351-A/21
PD 18-SEP-2001
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PR 03-MAR-1997 US 60/039762,02-MAR-1998 US 09/033333 PI
DE CHAO YU,DANIEL R,HENDERSON,BRIC R,SCHUUR,HENRY G LAMPARSKI PC
CI2N15/86,C12N5/10,A61K48/00,A61K47/48,C12Q1/70,C12N11/08 CC
Strandedness: Single;
CC Topology: Linear;
CC Adenovirus vectors specific for cells expressing androgen CC
receptor and
CC methods of use thereof
FH Key Location/Qualifiers
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Db |||||||
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Db |||||||

RESULT 4
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LOCUS BD195488 307 bp DNA linear PAT 17-JUL-2003
DEFINITION Adenovirus vectors containing heterologous transcription regulatory
elements and methods of using same.
ACCESSION BD195488
VERSION BD195488.1 GI:33005258
KEYWORDS JP 2002514074-A/9.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE
1 (bases 1 to 307)
Henderson,D.R., Yu,D.C. and Lamparski,H.G.
AUTHORS Adenovirus vectors containing heterologous transcription regulatory
TITLE elements and methods of using same
JOURNAL Patent: JP 2002514074-A 9 14-MAY-2002;
COMMENT
OS Unidentified
PN JP 2002514074-A/9
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PD 14-MAY-2002  
PF 03-MAR-1998 JP 1998538674  
PR 03-MAR-1997 US 60/039762, 03-MAR-1997 US 60/039763 PR  
04-AUG-1997 US 60/054523, 02-MAR-1998 US 09/033556 PI DANIEL  
R HENDERSON, DE CHAO YU, HENRY G LAMPARSKI PC  
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CC Adenovirus vectors containing heterologous transcription CC  
regulatory  
elements and methods of using same  
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Adenovirus vectors specific for cells expressing carcinoembryonic  
antigens and methods of use thereof.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 307)  
Lamparski, H.G., Henderson, D.R. and Schuur, E.R.  
Adenovirus vectors specific for cells expressing carcinoembryonic  
antigens and methods of use thereof  
Patent: JP 2002514075-A 19 14-MAY-2002;  
CALYDON INC  
OS Unidentified  
PN JP 2002514075-A/19  
PD 14-MAY-2002  
PF 03-MAR-1998 JP 1998538697  
PR 03-MAR-1997 US 60/039763, 02-MAR-1998 US 60/039763 PI  
HENRY G LAMPARSKI, DANIEL R HENDERSON, ERIC R SCHUUR PC

C12N15/86, C12N5/10, A61K48/00, A61K47/48, C12Q1/70, C12N11/08 CC  
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CC Topology: Linear;  
CC Adenovirus vectors specific for cells expressing CC  
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DB 301 TGATTAA 307

RESULT 6  
BD217928  
LOCUS  
DEFINITION  
BD217928 307 bp DNA linear PAT 17-JUL-2003  
Adenovirus vector specific to cell expressing alpha-fetoprotein and  
method of using the same.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
1 (bases 1 to 307)  
Little, A.S., Lamparski, H.G., Henderson, D.R. and Schuur, E.R.  
Adenovirus vector specific to cell expressing alpha-fetoprotein and  
method of using the same  
Patent: JP 2002516568-A 22 04-JUN-2002;  
CALYDON INC  
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PN JP 2002516568-A/22  
PD 04-JUN-2002  
PF 03-MAR-1998 JP 1998538676  
PR 03-MAR-1997 US 60/039597, 02-MAR-1998 US 09/033428 PI  
ANDREW S LITTLE, HENRY G LAMPARSKI, DANIEL R HENDERSON, ERIC R PI  
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PC C12N15/86, C12N7/00  
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DEFINITION Sequence 22 from patent US 6585968.  
ACCESSION AR349303  
VERSION AR349303.1 GI:33750029  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 307)  
AUTHORS Little,A.S., Henderson,D.R., Schuur,E.R. and Lamparski,H.  
TITLE Adenovirus vectors specific for cells expressing alpha-fetoprotein  
and methods of use thereof  
JOURNAL Patent: US 6585968-A 22 01-JUL-2003;  
Cell Genesys, Inc.; Foster City, CA  
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VERSION AR451690.1 GI:42682805  
KEYWORDS  
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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 307)  
AUTHORS Henderson,D.R. and Schuur,E.R.  
TITLE Tissue specific adenoviral vectors  
JOURNAL Patent: US 6676935-A 22 01-FEB-2004;  
Cell Genesys, Inc.; Foster City, CA  
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VERSION AR451690.1 GI:42682805  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 307)  
AUTHORS Henderson,D.R. and Schuur,E.R.  
TITLE Tissue specific adenoviral vectors

JOURNAL Patent: US 6676935-A 10 13-JAN-2004;  
Cell Genesys, Inc.; South San Francisco, CA  
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DEFINITION Sequence 61 from patent US 6676935.  
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VERSION AR451740.1 GI:42682855  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 307)  
AUTHORS Henderson,D.R. and Schuur,E.R.  
TITLE Tissue specific adenoviral vectors  
JOURNAL Patent: US 6676935-A 61 13-JAN-2004;  
Cell Genesys, Inc.; South San Francisco, CA  
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ACCESSION AR474487
VERSION AR474487.1 GI:42713368
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Yu, D.-C., Li, Y., Little, A. S. and Henderson, D. R.
TITLE Cell-specific adenovirus vectors comprising an internal ribosome
entry site
JOURNAL Patent: US 6692736-A 17 FEB-2004;
Cell Genesys, Inc.; South San Francisco, CA
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Best Local Similarity 100.0%; Pred. No. 1e-83;
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ACCESSION AR635125
VERSION AR635125.1 GI:59793252
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 307)
AUTHORS Yu, D. C. and Henderson, D. R.
TITLE Adenovirus vectors containing cell status-specific response
elements and methods of use thereof
JOURNAL Patent: US 6900049-A 7 31-MAY-2005;
Cell Genesys, Inc.; San Francisco, CA
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DEFINITION Sequence 7 from patent US 6900049.
ACCESSION AR669908
VERSION AR669908.1 GI:67608182
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REFERENCE 1 (bases 1 to 307)
AUTHORS Yu, D. C. and Henderson, D. R.
TITLE Adenovirus vectors containing cell status-specific response
elements and methods of use thereof
JOURNAL Patent: US 6900049-A 7 31-MAY-2005;
Cell Genesys, Inc.; San Francisco, CA
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REFERENCE 1 (bases 1 to 307)
AUTHORS Yu, D.-C., Zhang, H. and Henderson, D. R.
TITLE Human and mouse uroplakin II gene transcriptional regulatory
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JOURNAL Patent: US 6852528-A 3 08-FEB-2005;
Cell Genesys, Inc.; San Francisco, CA
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DEFINITION Sequence 7 from patent US 6900049.
ACCESSION AR669908
VERSION AR669908.1 GI:67608182
KEYWORDS
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REFERENCE 1 (bases 1 to 307)
AUTHORS Yu, D. C. and Henderson, D. R.
TITLE Adenovirus vectors containing cell status-specific response
elements and methods of use thereof
JOURNAL Patent: US 6900049-A 7 31-MAY-2005;
Cell Genesys, Inc.; San Francisco, CA
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ACCESSION AJ293912  
VERSION Au293912.1 GI:15485529  
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SOURCE Human adenovirus type 2  
ORGANISM Human adenovirus type 2  
REFERENCE 1 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus. Borchering, F. and Pring-Akerblom, P.  
TITLE Adenoviruses of subgenus c with different organ tropism  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3454) Borchering, F.  
AUTHORS Direct Submission  
TITLE Submitted (01-SEP-2000) Borchering F., Institut fuer Virologie, Medizinische Hochschule Hannover, Carl-Neuberg-Str. 1, 30625 Hannover, GERMANY  
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Qy	121	CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATTATTATGTGGCTTATTG	180
Db	2211	CATGTGGTGGTTTCCATAGCGCTTATGTTTGTGGCTTATTATTATGTGGCTTATTG	2270
Qy	181	TTGGCTAAAGCGCAGACGCGCCAGACCCCACTCTATAGCCCTATCATTTGTGCTCAACCC	240
Db	2271	TTGGCTAAAGCGCAGACGCGCCAGACCCCACTCTATAGCCCTATCATTTGTGCTCAACCC	2330
Qy	241	ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA	300
Db	2331	ACACAAATGAAAAAATTCATAGATTGGACGGTCTGAAACCATGTTCTCTCTTTTACAGTA	2390
Qy	301	TGATTAA 307	
Db	2391	TGATTAA 2397	

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